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New mutant glucose isomerase enzymes -

Obtd. by site-directed mutagensis of gene from Actinoplanes

obtd. by site-directed mutagensis of gene from Actinoplanes

Example, Floure 19, 56pp; English.

The invention is a novel mutant glucose isomerase (GI) enzyme with

Improved properties thru As substitu. The GI is pref. derived from

Actinoplanes missouriensis. The substitu. is Lys for Arg.

Or vice versa. Specific Lys or Arg residues are identified and site-

directed mutagenesis of the DNA sequence encoding the GI is performed.

The novel mutant gi shows 55 per cent or more sequence homology with the

As sequence of WT A. missouriensis GI. Compared to wr enzyme it shows

Chipher conversion performance and improved thermostability and pH

stability. The example concerns the cloning and sequencing of

GI from other bacterial strains. Fig 21 displays the AA SOS to
                                                        S. avermitilis BCK
S. avermitilis bkd
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sram coding sequen
Tylactone synthase
BamHI J-I fragment
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02-FBB-1991 (first entry)
Complete gene sequence of wildtype (WT) Streptomyces murinus
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Pred. No. 1.7e-117;
0; Mismatches 112;
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17-JUL-1989; 201892.
04-NOV-1988; EP-402789.
(KONN) Gist-Brocades NV (Plan-).
Luiten RGM, Quax WJ, Schuurhulzen PW, Mrabet N;
WPI; 90-016368/03.
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Site-directed mutagenesis; glucose isomerase;
high fructose corn syrup; ss.
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Sequence 1164 BP; 178 A; 445 C;
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                        Compugen Ltd
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            GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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V32494; V32494; 21-SEP-1998 (first entry) S. griseofuscus glucose isomerase encoding

439 180 499 240 300 619 619 799 919 379 357 477 597 9 replacing part of amino acid in specific position of amino acid sequence Example 1; Fig 3; 7pp; Japanese.

Example 1; Fig 3; 7pp; Japanese.

This DNA encodes a Streptomyces glucose isomerase. This glucose isomerase is used to create a mutant with improved heat resistance which comprises replacing an amino acid in a specific position of t isomerised sugar.

Sequence. The glucose isomerase is useful for the preparation of Sequence 1164 Bp; 181 A: 263 atgaactaccagcccaccccgaggacaggttcaccttcggcctgtggaccgtcggctgg caggggcgggaccccttcggcgacgccacgcgtcccgccttcgacccggtcga---cgtg ttoggggggtccgacaccgagggggggggaggtcaaggggttcgtcagggggttcgac gagggcgcgcggtgccgccaaggacgtgcgtgcggccctggaccgcatgaaggag gagocomagocogamogagocogogogogacatectgotocomecategocomecogococo gccttcatcgagcgcctggagcgccccgagctgtacggtgtcaaccccgaggtgggccac cagoggotggcogaactgggcgcotacggagtgacottccacgacgacgactgatccc TTCGGGTCGTCCGACACCGAGCGCGAGTCGCACATCAAGCGGTTCCGCCAGGCCCTGGAC . 6 61.2%; Score 946.2; DB 1; Length 1164; 90.0%; Pred. No. 1.2e-116; sugar; ss.
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/transl_except= (pos:1138. il40, aa:Cys)
/product= "Glucose isomerase" mutant; Indels thermostable; 0; Mismatches 108; heat resistance; Conservative 07-APR-1998. 12-SEP-1996; 262370. 12-SEP-1996; JP-262370. (GODO) GODO SHUSEI KK. WPI: 98-264846/24. P-PSDB: W63617. 1somerase; Best Local Similarity Matches 1050; Conserv isomerised su Streptomyces Query Match 323 61 740 478 538 380 121 440 181 200 241 260 301 620 358 980 418 800 860 ò à ద

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Disclosure: ; 114pp; English.

New in the patent are muteins of the protein encoded by n91083. These muteins are used to convert glucose to fructose, and xylose to xylulose, eg in mfr. of sweeteners. Compared with native xylose the muteins have different chemical and thermal stability, kinetic constants, specificity and/or lower optimum PH. Amino acid substitution sites are selected by first determining, from the crystallographic structure, the phi and psi angles, then screening these for values within the specified ranges eg a site which has a phi backbone configuration angle -40 to -90 degrees when psi configuration angle is 0 to -60 degrees, ven psi configuration angle is 0 to -60 degrees.
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14-JUL-1990 (first entry)
DNA sequence encoding Streptomyces rubiginosus xylose isomerase
Streptomyces rubiginosus xylose isomerase gene; mutein; fructose;
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22-MAR-1988; US-171693, US-084479.
(CETU) Cetus Corp (UYOR-).
WPI: B9-068875/09.
P-PSDB; P94687.
Increasing stability of proteins by specific aminoacid replace where aminoacid introduced decreases configuration entropy of unfolding of protein
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Key Location/Qualifiers
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distortion of the 3-D protein structure, so that the substitution decreases the configurational entropy of unfolding CEU; or replacing a Gly residue having a negative phi angle with Ala, also decreasing t
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                                                                                                        Gaps
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                                                                                                      9
                                                                                 Length 1167;
                                                                                                      Indels
                                               156
                                                                              Score 931.8; DB 1;
Pred. No. 9.3e-115;
0; .Mismatches 127;
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                                               403
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                                                                             Query Match 60.3%;
Best Local Similarity 88.6%;
Matches 1034; Conservative
                                               180
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GCCTCGGCGGCCGGCTGCATGCGCAACTACCTGATCCTCAAGGAGCGTGCGGCGGCGCCTTC
                                                   cgtgccgacccggaggtccaggaggccctgcgtgccgcccggctcgaccagctcgccgag
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Glucose isomerase gene from Streptomyces
Glucose isomerase; Streptomyces; DNA.
Streptomyces
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20-AUG-1990 (first entry)
Nucleotide sequence of D-glucose isomerase (EcoAmi(DSM) GI) from
Actinoplanes missouriensis (DSN 43046) produced by engineered E.
Actinoplanes missouriensis (DSM 43046); D-glucose isomerase;
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Bloogically active modified protein prodn. -
comprises substituting arganine residue for lysine in starting protein
; Fig 16, 64pp; English.
Its starting protein is native D-glucose isomerase. It is a portion of
vectors pMa5-GI and pMc5-GI used in the process of making a modified
D-glucose isomerase gene. The method involves substituting one or more
Lys with Arg, or vice versa, at a site which can accommodate such a
substitution without altering the biological activity. The resulting
gene has enhanced thermostability and increased resistance towards
chemical modification
                       316
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Sequence of the rightward promoter (Pr) of bacteriophage lambda Actinophanes missouriensis D-glucose isomerase (g1) gene Actinophanes missouriensis DSM 43046); D-glucose isomerase; D-xylose isomerase; D-xylose ketol-isomerase; plasmid pMa5-GI; plasmid pMc5-GI; transcriptional unit.

Bacteriophage lambda and Actinoplanes missouriensis.

Key
Location/Qualifiers

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137. .1525
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/note="DNA of Actinoplanes missouriensis"
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Mrabet N, Lasters I, Stanssens P, Mathyssens G, Wodak S,
WPI; 90-052789/08.
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Pred. No. 2e-71;
0; Mismatches 324;
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17-JUL-1989; EP-201893, EP-201539.
                                                                                                                                                                                                                                                                                                                  BP.
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Local Similarity 71.0%;
les 861; Conservative (
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                                                                                                                                   Biologically active modified protein prodn. -
Comprises substituting arganine residue for lysine in starting protein
Fig 15; 64pp; English.
It encodes D-glucose lasomerase from Actinoplanes missouriensis
(DSM 43046). It is genetically engineered to code for a mutein
that has increased thermostability and increased resistance
towards chemical modification. It is used in an example of
the method, which is claimed, where one or more Lys are substd. by Arg o.
vice verse, at a site which can accommodate such a substitution without
altering the biological activity. Lysine-253 was substd. by Arg.
Sequence 1185 BP; 210 A; 429 C; 377 G; 169 T;
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                                                                                                                                                                                                                                                                             Length 1185;
                                                                                                                                                                                                                                                                            38.7%; Score 598.8; DB 1; Length 72.0%; Pred. No. 2.7e-71; ive 0; Mismatches 302; Indels
                                                                                                         Wodak S,
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                                                          21-FEB-1990.
17-JUL-1989; 201893.
17-JUL-1989; EP-201893, EP-201539.
(KONN) Gist-Encades NV (PLAN-).
MINDER N. LISSTERS I, Stanssens P, Mathyssens P-PSDB; R052289/08.
isomerase; D-xylose ketol-isomerase.
                     Location/Qualifiers
1. .1188
                                                                                                                                                                                                                                                                                       Best Local Similarity 72.0 Matches 847; Conservative
 D-xylose ison
Actinoplanes
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isomerase; Actinoplanes missouriensis;
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obtd. by site-directed mutagensis of gene from Actinoplanes
missouriensis, used for prodn. of high fructose corn syrups
missouriensis, used for prodn. of high fructose corn syrups
missouriensis, used for prodn. of high fructose corn syrups
missouriensis, novel mutant glucose isomerase (GI) enzyme with
improved properties thru AA substitn. The GI is pref. derived from
Actinoplanes missouriensis. The substitn. is Lys for Arg.
or vice versa. Specific Lys or Arg residues are identified and site-
directed mutant gi shows 65 per cent or more sequence homology with tl
AA sequence of WT A. missouriensis GI. Compared to wt enzyme it shows
higher conversion performance and improved thermostability and pH
stability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete gene sequence of wildtype (WT) Actinoplanes missouriensis glucose isomerase (GI)
cggctgggagggtccgcgccacttcgacttcaagcccccgcggagccgaggacatcgacgg
                                                                                                                                                                                                                                                                                                                                                                                                                      GGCGTACGACGGACCCCGTCACTTCGACTACAAGCCGTCCCGTACCGAGGACTACGACGG
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04-NOV-1988; EP-402789.
(KONN) Gist-Encoades NV (Plan-).
Lulten RGM, Quax WJ, Schuurhuizen PW, Mrabet
WPI; 90-016368/03.
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EP-483691-A
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Matches 788;
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                  27;
      Length 1182;
                  Indels
     Score 598.4; DB 1;
Pred. No. 3e-71;
0; Mismatches 301;
     tch 38.7%;
al Similarity 72.1%;
846; Conservative
     Query Match
Best Local S
Matches 846
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PERMED: R2263.

WPP: 92-152788/19.

P-PSDB; R22623.

Trocked in - expressed on large scale and used to produce conc.

fructose from glucose

fructose from glucose

Claim 1; Frg 1-3; 24pp; English.

To obtain the DNA sequence of the xylose isomerase gene from Thermus aquaticus genomic DNA from T. aquaticus was digested by SacI and the gel neutralised. The DNA was denatured and the gel neutralised The DNA fragments were blotted onto a nylon membrane and hybridised with a labelied 287 base Bgl fragment of a Streptomyces griseofuscus 5-41 xylose isomerase gene. A single digested with SacI. This was used to transform E. Coli JM109 and transformants selected using the above probe. A 1.8 kb SacI transformants selected using the above probe. A 1.8 kb SacI cransformants and subcloned into E. Coli JM109 using pUC118 and pUC119. These fragments were then sequenced. The gene allows large scale expression of T. aquaticus xylose isomerase which is used in the prob. Of fructose at higher temperatures than those previously problem. Colouries and highly conc. fructose which is free of coloured by prods. Such as psicose, usually formed when the pH of the reaction mixtures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              445
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                                                                                                                                                              1089 GTTCGAGGACTACGACGCCGAGGCGCCCAAGGGCTTCGGCTTCGTCAAGCTGAAA
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----cgccgagcccaccgcggccgacggcctgcaggccctgctggccgaccgcaccgc
                               1029 GAAGACCCCGACCCTGAACCCGGGCGAGGGATACGCCGAGCTGCTCGCCGACCGCAGCGC
                                                                                                                     ggccgcgcgcgtggcttcgagcgcctcga
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Pred. No. 4.6e-56;
0; Mismatches 467; Indels 6;
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Thermus aquaticus xylose isomerase gene.
Large scale; recombinant; colourless; fructose;
Thermus aquaticus.
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Dekker K, Sakaguchi K, Udaka S, Yamagata
WPI; 92-152378/19.
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288. .1461
/*tag= a
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07-MAR-1991; JP-067967.
24-JUN-1991; JP-178698.
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Sequence 1805 BP;
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The specification describes antisense oligonucleotides (X52869-X55271)

directed against at least 2 mRNAs selected from target genes, coding and
con-coding regions of RNAs corresponding to target genes, coding and
con-coding regions of RNAs corresponding to target genes, coding
initiation codons, genomic flanking regions, intron-exon borders, the
confidence of the 3'-end and the juxta-section between coding and non-coding
confidence and all segments of RNAs encoding proteins associated with one
cor more diseases, conditions or mixtures. The antisense oligonucleotides (specifically X55180-271) can be used for the antisense
creatment of diseases and conditions. Typical diseases and conditions
creatment of diseases and conditions. Typical diseases and conditions
are those associated with impaired respiration and inflammation,
allergic rhinitis, acute asthma, allergies, asthma, impeded respiration,
crespiratory distress syndrome, pain, cystic fibrosis, pulmonary
pulmonary diseases (COPD), and cancers wich as leukemias, lymphomas,
cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic
cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic
metastasized to the lungs, including breast and prostate cancer.
Squence 114955 BP; 6071 A; 29417 C; 36712 G;
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Human adenosine Al receptor antisense oligonucleotide fragment.

Human adenosine Al receptor antisense oligonucleotide fragment.

Antisense oligonucleotide; multiple target; antisense treatment;

Impaired respiration; inflammation; lung disease;

pulmonary vasoconstriction; inflammation; allergic rhinitis;

acute asthma; allergy; asthma; impeded respiration;

respiratory distress syndrome; pain; cystic fibrosis;

pulmonary hypertension; pulmonary vasoconstriction; emphysema;

chronic obstructive pulmonary disease; leukenia; lymphoma; carcinoma;

colon cancer; breast cancer; lung cancer; pancreatic cancer;

hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
1491 AGGCCCTGGTGCTGGACGAGGGGTAGAAAGCGCGCTGAGGCCCGGGCCGGGTTACCCC 1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94 tcagggggctctgacctgcggcttcacgctatgccggggcctgtggggccccgggggtgcggac 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antisense oligonuclectides used in treatment of, e.g. pulmonary vasoconstriction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      154 ccggcccggcccgtttctgcttccgcgttcccttcccagggacgcgctcggcatactaat
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                                                                                                                                                                                                                  X53491 standard; DNA; 114955
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09-JUN-1998; US-093972.
17-SEP-1997; US-059160.
(UYEC-) UNIV EAST CAROLINA.
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104782 NNHNNNSCGCCCVGGCCVGCGGNNHNNNSGCGCCCVGGCCVGCGGNNHNNNSCGCGCCCV 104723
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                             104902 VGGCCVGCGNHHNNNSGGCCVGCGGNHHNNNSVGGCCVGCGGNHNNNSCVGGCCVGCGG 104843
                                                                                                             Db 104842 NNHNNNSCCVGGCCVGCGGNNHNNNSCCCVGGCCVGCGGNNHNNNSGCCCVGGCCVGCGG 104783
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Protease Tap-negative cells were transformed with a S. lividans 66 genomic library and screened with APA-beta-naphthylamide to isolate colonies contg. genes (099365-68) for novel proteases P5-4, P5-6, P5-10 and P8-2 (R80505-08). Impaired expression of such proteases by Streptomyces hosts improves the quality, quantity and stability of excygenous gene products. 602 G; 221 T; Sequence 1821 BP; 238 A; 715 C; 602 G; 221 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             having impaired activity
                           103824 ACGCCCCAVGACGCCNNHNNNSGCCCGGCCCGACGCCGCAVGACGGCCNNHNNNSGCC
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                                                                                                                                                                                                                                                                                            S. lividans protease P5-6 gene.
Protease, metalloendoproteinase; tripeptidyl aminopeptidase;
protease-deficiancy; protein secretion; ds.
Streptomyces lividans.
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Matches 529; Conservative
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Soostmeyer G,
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29-JUN-1995.
22-DEC-1994; U14772.
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(CANG-) CANGENE CORP.
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494068;
19-MAR-1999 (first entry)
Clone P5-6 encoding an aminopeptidase designated SlpD.
Clone P5-6 incoding an aminopeptidase; TAP; N-terminal cleavage; protein production; GM-CSF; interleukin-3; IL-3; IL-3; IL-6; EPO; tumour necrosis factor; TNF; SCF; IL-7; IL-2; P5-6; SlpD; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptomyces tri:peptidyl aminopeptidase - useful for removing N-terminal pro-peptide from secreted proteins
Bxample 25; Fig 25A-C; 83pp; English.

Example 25; Fig 25A-C; 83pp; English.

The present sequence encodes an aminopeptidase designated SlpD. The specification also describes a tripeptidyl aminopeptidase (TAP) of Streptomyces. The aminopeptidase is endogenous to Streptomyces and cleaves an N-terminal sequence of X-pro-Y, where X is an alibhatic or hydroxy amino acid and Y is an aliphatic, hydroxy or sulphur-containing amino acid. The TAP of Streptomyces are useful in the production of proteins, such as GM-CSF, interleukin-3 (IL-3), Sequence 1821 BP; 283 A; 715 C; 602 G; 221 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     543 geracecesecaagerecececearaceaearecagesecereaecececeses
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44.8%; Pred. No. 7.7e-06;
tive 0; Mismatches 625; Indels
                                                                                                                                                                                                                                                                                                                                         05-JAN 1999.
24-JUN-1994; 265310.
24-JUN-1994; US-265310.
23-DUC-1993; US-173508.
(CANG-) CANGENE CORP.
Bartfeld D, Butler MJ, Garven S, Hadary D, Jenish DL,
Krieger TJ, Krygsman P, Malek LT, Scostmeyer G, Walczyk
P-PSDB; W87799.
Location/Qualifiers
104. 1723
104. 1723
/*tag a
/product protease
104. 244
                                                                                                                                                                                          /*tag= b
245. 1720
/*tag= c
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Matches 529; Conservative
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/product acyl carrier protein used by the PKS /note "gene N (specifically claimed)" complement (16453. .16935)
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                                                                                                                                                                                                                           gene
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/note- "gene P (specifically claimed)"
17903. .18898
                          /product- unknown non-membrane protein
/note- "gene E (specifically claimed)"
7344. .8997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= q | /*tag= c/product= cyclase/dehydrase related to /product= "gene Q (specifically claimed)" 18895. .19839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product- cyclase/dehydrase related to
/note- "gene R (specifically claimed)"
complement (19990. .20907)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product= putative hemiketal dehydrase
/note= "gene O (specifically claimed)"
17088. .17903
                                                                                                                                                                                                                                                                                                                                                                                   /product acyltransferase
/note gene K (specifically claimed)"
13409. 14686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product PKS chain length factor/note "gene M (specifically claimed)"
                                                                                                                                                                                                                                                                                               /note= "gene I (specifically claimed)"
11809. .12066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product= quinone-forming hydroxylase
/note= "gene T (specifically claimed)"
complement (22505. .22179)
                                                                                                   /product- putative efflux pump
/note- "gene F (specifically claimed)
9164. .10012
                                                                                                                                                                           /note= "gene G (specifically claimed)
                                                                                                                                                                                                                       /product- translationally coupled to force- "gene H (specifically claimed) complement (10618. .11628)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "gene S (specifically claimed) complement (20904. 22094)
'note "gene D (specifically claimed)
                                                                                                                                                                                                                                                                                                                                           /product= acyl carrier protein
/note= "gene J (specifically claimed)
complement (12154. .13209)
                                                                                                                                                             /product - transcription activator
                                                                                                                                                                                                                                                                                 /product= homologue of fabH
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/product= quinor
/note= "gene T (
            6533. .7183
/*tag= e
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12-NOV-1997.
02-MAY-1997; 107329.
07-MAY-1996; US-016753.
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 1176 CGATGTACGACGAGGGCGCCTGGCAGCTGCGCGAGTCCCTCACCTCGGCGATCAAGG 1235
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 acgacatccggttcgccatcgagcccaagccgaacgagccgcggcgacatcctgctgc
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                                                         ccaccatoggccacgcgctcgccttcatcgagcgcctggagcgccccgagctgtacggtg
                                                                          900 tcaaccccgaggtgggccacgaggcaggtggccggcctgaacttcccgcacggcatcgcgc
                                                                                                                                                                                                         AGAAGGACGGTGCGGGCCTGCTGTCCTCTCCGACAGCTACTACGAGCGCGAGGCCGACG
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Streptomyces frenolicin gene cluster.
Frenolicin; antibiotic; feed additive, anticoccidial;
coccidiostatic; efflux pump; butyrate starter synthase;
polyketide synthase; PKS; hemiketalase; ketoreductase; cyclase;
dehydrase; ketoreductase; hydroxylase; Streptomyces roseofulvus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product- protein with 6 membrane-spanning
/note- "gene C (specifically claimed)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  636. .2948
/*tag= a
/*product= 80 kDa non-membrane protein
/note= "gene A (specifically claimed)"
2945. .3916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               *tag= b
/product= membrane protein
/forote= "gene B (specifically claimed)'
4020. .4844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tcgaccagctcgccatggaccacctgctgggggcgccgcggc 1420
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T93095;
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15873 CCTCGTGCCCCCGGCCGTCCACCTCGACGAGGTCGATCCCGCGGTACGGCCTCGACCTCGT 15932
15633 CCTCGAACGCGCCGCGCGCCTCGCCCTCGCCGACGCGGGCCTGGCACCCGGGGACGTCGA 15692
                                                                                                                                                                                                                                                                                                                                                                                                                                     caccgogtacgaggacttcgacgtggacgcggcgcgcgcgcgcatggccttcgagcgct
                                                                                                                                                                                                                                                     GCGCGCGCTCTTCGGCCCCCGGCGCGTTCCGGTGAGCGTGCCGAAGACCCAGACCGGGCG
                                                                                                                                                                                                                                                                                                                   1261 getegaceagetegeegageecacegeggeegaeggeetgeaggeeetgetggeegaeeg
                                                                                                                        15693 CGTCGTCTTCGCGGACGCGGCGGCGTCCCCGCCGCCGACGCCGCAAGGCCGCCGCCTT
                                                                 ggacatcgacggcgtgtgggcctccgcgggccgggtgcatgcgaactacctgatcctgaa
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15-pur-1998 (first entry)
Streptomyces roseofulvus; frenolicin gene cluster; frenolicin antibiotic; ss.
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/note= "encodes protein given in W55807"
complement (10618, .11628)
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note= "encodes protein given in W55808"
1809. .12066
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complement (12154. .13209)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /traísl_except= (pos:2945. .2947,aa:Met)
/note= "encodes protein given in W55801"
4020. .4844
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/note= "encodes protein given in W55802"
4841. .6415
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9164. .10012
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/note= "encodes protein given in W55806"
complement (10105. .10621)
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V25925 standard; CDNA; 24379 BP.
AC V25925;
DF 15-JUL-1998 (first entry)
DE Streptomyces roseofulvus; frenoli
KW Streptomyces roseofulvus; frenoli
KW antiblotic; ss.
CS Streptomyces roseofulvus; frenoli
KW antiblotic; ss.
CS Streptomyces roseofulvus; frenoli
KW Streptomyces roseofulvus; frenoli
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                                                                                                               Streptomyces francisin gene cluster - useful for producing recombinant francisin antibiotics

recombinant francisin antibiotics

clust 1: Page 40-60; 66pp; English

This DNA sequence comprises the Streptomyces franciscin gene

cluster containing specifically claimed coding sequences (genes

A-U) that respecitively encode 21 proteins (see W34199-219) involved

in franciscin synthesis. The genes can be divided into 5

subclusters: (1) genes A, B, C, D and F encode an efflux pump; (2)

subclusters: (1) genes A, B, C, D and F encode an efflux pump; (2)

subclusters: (1) genes A, B, C, D and F encode an efflux pump; (2)

subclusters: (3) genes A, B, C, D and F encode an efflux pump; (2)

R encode a hemiketalase, a ketoreductase and cyclases/dehydrases;

L, M and N encode polyketide synthases; (4) genes O, P, O and

R encode a hemiketalase, a ketoreductase and cyclases/dehydrases;

C, M and N encode polyketide synthases; (1) genes

C, D and F encode a polyketide synthases; (1) genes

C, M and N encode polyketide synthases; (1) genes

C, M and N encode polyketide synthases; (1) genes

C, M and N encode polyketide synthases; (1) genes

C, M and N encode polyketide synthases; (1) genes

C, M and N encode polyketide synthases; (1) genes

C, M and N encode polyketide synthases; (1) genes

C, M and N encode polyketide synthases; (1) genes

C, M and N encode polyketide synthases; (1) genes

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C, M and N encode polyketide synthases; (1) genes

C, M and N encode polyketide synthases; (1) genes

C, M and N encode polyketide synthases; (1) genes

C, M and N encode polyketide synthases; (1) genes

C, M and N encode polyketide synthases

C, M and N encode synthases

C, M and N encode polyketide synthases

C, M and N encode polyketide synthases

C, M and N encode polyketide synthase
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44.5%; Pred. No. 1.5e-05;
Live 0; Mismatches 515; Indels
<u>ω</u>,
HOFF ) HOFFMANN LA ROCHE & CO AG
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Matches 415; Conservative
                          Reeves CD, Soliday CL;
WPI; 97-538619/50.
P-PSDB; W34199-W34219.
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Platenolide synthase gene cluster.
Platenolide synthase gene cluster; platenolide production; srmG gene; .
multi-functional protein; macrolide antiblotic; spiramycin; ss.
                      CCACCGCGAGATCCGCAAACTCTGGACCGAGGGCCCGGCCCGCGTCAGGGGTCTACGAGTC 15212
                                                                15273 CCCCGGCGCCGTCGTCGTGGCCGACCAGGCGGCGGCCTCGACGCCCTCGGCCAGGCCCG
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/note= "ORF1 encodes protein shown in W23716"
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"ORF2 encodes protein shown in W23717"
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350. .14002
/*tag= a
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The present sequence represents a frenolicin gene cluster from Streptomycas roseofulus. The present intention describes: (1) a cettor containing the frenolicin gene cluster DNA sequence operably connected to an expression control sequence; (2) a host cell remoistered by the above vector; (3) a protein coded by the above DNA cransformed by the above vector; (3) a protein coded by the above DNA composition or transformed for the preparation of frenolicin or a biosynthetic intermediate for it in which the above cell is cultured and frenolicin or its biosynthetic intermediate is isolated from the culture or the cell; (5) a method for the preparation of frenolicin B coulture or the cell; (5) a method for the preparation of frenolicin B composition by mixing frenolicin with other components.

Creamolicin B is useful as an antibiotic: (8499 G; 3011 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15093 GCTGCCCGAGTACGGGGCGAGCGCCGTCACCTCCAACGCCACCGGCGCGTTCGAGTTCAC 15152
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/transl_except= (pos:22037. .22035.aa:Arg)
/transl_except= (pos:22034. .22032.aa:Thr)
/transl_except= (pos:22031. .22029.aa:Lys)
/note= "encodes protein given in W55819"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /transl_except= (pos:20907. .20905,aa:Met)
/note= "encodes protein given in W55818"
complement (20904. .22094)
                                                              (pos:13409. .13411,aa:Met)
protein given in W55811"
                                                                                                                                                                                                                                                                         /transl_except= (pos:16935. .16933.aa:Met)
/note= "encodes protein given in W55814"
17088. .18903
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protein given in W55810'
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07-MAY-1997, 116652.

04-APR-1996, US-042935.

07-MAY-1996, US-016753.

(HOFF) HOFFMANN LA ROCHE & CO AG F.

WPI: 98-279231/25.

P-PSDB; W55800-W55819.
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Matches 415; Conservative
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PPSDB; W2316-W33720.

DNA encoding Streptomyces ambofaciens platenolide synthase domain - production of spiramycin-related polyketide antibiotics production of spiramycin-related polyketide antibiotics claim 9; Pages 8-33; 81pp; English.

This sequence represents the platenolide synthase gene cluster of the invention. This sequence encodes the related from Streptomyces ambofaciens. This sequence encodes the multi-functional proteins which direct the synthesis of the polyketide platenolide. Platenolide is the basic building block of the macrolide antibiotic spiramycin. The DNA can be used to produce compounds exhibiting antibiotic activity based on the platenolide structure, concluding specifically the macrolide antibiotic spiramycin analogues and derivetives. Modifications of the platenolide synthase DNA sequence can be made so as to change the number and type of carboxylic alide incorporated into the growing polyketide chaim and to change the kind of post-condensation processing that is conducted.

Sequence 44377 BP; 4965 A; 15552 C; 17381 G; 6479 T;
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Pred. No. 0.00014;
0; Mismatches 413; Indels 0;
                                   .except- (pos:20111. .20113, aa:Met) "ORF3 encodes protein shown in W23718" .36071
                                                                                                                     "ORF4 encodes protein shown in W23719"
                                                                                                                                                                                  "ORF5 encodes protein shown in W23720"
                                                                                                                                                                                                                                                                                                        Kuhstoss SA, Rao RN, Richardson MA;
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.31284
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Matches 333; Conservative
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production of tylosin-related polyketide compounds

Transpired by Azaron Faratives fradiae tylactone synthase domain - for
production of tylosin-related polyketide compounds
Example 2; Pages 10-134; 220pp; English.

This sequence represents the platenolide synthase gene cluster of the invention. This sequence is referred to as the srmG gene, and was invention. This sequence encodes the multi-functional proteins which direct the synthesis of the polyketide platenolide. Platenolide is the basic building block of the macrolide antibiotic spiramycin. This sequence was used along with the tylG gene antibiotic spiramycin. This sequence was used along with the tylG gene is the tylactone synthase gene cluster of the invention. The tylG gene is the tylactone synthase gene cluster of the invention. The tylG gene sequence was isolated from Streptomyces fradiae, and encodes multifunctional proteins which direct the synthesis of the polyketide tylactone. Tylactone is the basic building block of the antibiotic tylactone. Tylactone can be used to transform S. ambofaciens con tacking the srmG ORF1 sequence, or S. fradiae lacking the tylG ORF1
30484 AGCCTCCAGCGGCGCTTCGCCCGCAGCGGCTTCCCGCCCCTGTCCGCCACGCTGGGCGCCC 30543
                                                                                                                                                            GCGCTGTTCGACGCCGCCCTGCGGGTCGACGACGCCGTGCAGGTCCCCATGCGGTTCGAC 30603
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Tylactone synthase gene cluster; tylG gene; multifunctional protein; platenolide synthase gene cluster; tylG gene; multifunctional protein; platenolide synthase gene cluster; platenolide production; srmG gene; polyketide; tylactone synthesis; antiblotic; tylosin; ss. Streptomyces ambofaciens.
                                                                                    geogeetteegtgeegaeeeggaggteeaggaggeeetgegtgeegeeeggetegaeeag
                                                                                                                                                                                                                                                 ctcgccgagcccaccgcggccgacggcctgcaggcctgctggccgaccgcaccgcgtac
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14046 ..20036
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/note- "ORF3 encodes protein shown in W22608"
31329. .36071
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/note= "ORF5 encodes protein shown in W22610"
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Dehoff BS, Kuhstoss SA,
WPI; 97-418046/39.
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19-FEB-1997; 301056.
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sequence, so that they can produce polyketides. The DNA sequence can be modified so as to alter the type of carboxylic acids incorporated, the number of carboxylic acids incorporated and/or the post-condensation reactions performed, thereby resulting in novel tylosin-related
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                                                                                                                                                                                                                                                                                                                                                                                                                                 910
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                                                                                                                                                                                        Gaps
                                                                                                      6479 T;
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                                                                                                                                                    Query Match 5.5%; Score 85.2; DB 1; Length 44377; Best Local Similarity 44.6%; Pred. No. 0.00014; Matches 333; Conservative 0; Mismatches 413; Indels 0;
                                                                                                      17381 G;
                                                                                                    15552 C;
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Search completed: March 22, 2000, 23:35:09 Job time: 1116 sec

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Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 4, Sequence 1, Sequence 2, Sequence 2, Sequence 1, Sequence 2, Sequen

US-08-482-385A-5
US-07-736-17-20-17-

ALIGNMENTS

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APPLICANT: QUAX, WILHELMUS
APPLICANT: QUAX, WILHELMUS
APPLICANT: CUITEN, RUDOLF G.M.
APPLICANT: SCHURHUIZEN, PAUL W.
TITLE OF INVENTION: THEIR USE
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morilson & Foerster
STREET: 545 Middlefield Road, Suite 200
CITY: Menlo Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, veiscon SOFTWARE: Patentin Release #1.0, veiscon SOFTWARE: CURENT APPLICATION DATA: APPLICATION NUMBER: US/07/640,476
FILING DATE: 1991010
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kate H. Murashige
REGISTRATION NUMBER: 29,959
RECISTRATION NUMBER: 29,959
RECISTRATION NUMBER: 29,959
RECISTRATION NUMBER: 29,950
TELEFROME: (415) 327-2951
TELEPHONE: (415) 327-2951
TELEPHONE: (415) 327-2951
TELEFAX: 766141
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
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DSM 40091
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Patent No. 5376536
GENERAL INFORMATION:
APPLICANT: QUAX, WILHELMUS
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TYPE: NUCLEIC ACID
STRANDEDNESS: double
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ZIP: 94025
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FEATURE:
March 22, 2000, 23:05:43 ; Search time 44.32 Seconds
(without alignments)
4176.263 Million cell updates/sec
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Patent No. 521
Sequence 1, A
Sequence 3, A
Sequence 1, A
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/cgn2_6/ptodate/1/ina/5B_COMB.seq:*
/cgn2_6/ptodate/1/ina/5C_COMB.seq:*
/cgn2_6/ptodate/1/ina/5D_COMB.seq:*
/cgn2_6/ptodate/1/ina/PCTUS9_COMB.seq:*
/cgn2_6/ptodate/1/ina/PCTUS9_COMB.seq:*
/cgn2_6/ptodate/1/ina/PCTUS9_COMB.seq:*
                                          Compugen Ltd
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US-08-173-508-1
US-08-265-310-1
US-08-125-468-1
US-08-125-468-1
US-08-125-468-1
US-08-474-933-1
US-08-461-775-10
S212296-8
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                     GenCore version 4.5 Copyright (c) 1993 - 2000 Comp
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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 1000000
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                              /EC_number= 5.3.1.5
/product= "xylose isomerase (glucose isomerase)"
/evidence= EXPERIMENTAL
/standard_name= "D-xylose ketol isomerase"
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9
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                                                                                             Score 952.8; DB 1;
Pred. No. 8.8e-152;
0; Mismatches 112;
                      experimental
                                                                                               61.6%;
89.9%;
NAME/KEY: CDS

LOCATION: 1.1164

LIDENTIFICATION METHOD: e

OTHER INFORMATION: /EC_II

OTHER INFORMATION: /evic

OTHER INFORMATION: /evic

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                                                                                                        Best Local Similarity 89.9
Matches 1046; Conservative
                                                                                               Query Match
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MATHER MRABET, NADIR; LASTERS, IGNACE; STANSSENS, PATRICK APPLICANT: MRABET, NADIR; LASTERS, IGNACE; STANSSENS, PATRICK MATHER SENS, GASTON; WODAK, SHOSHANA; QUAX, WILHELMUS J.

TILLE OF INVENTION: METHODS AND MEANS FOR CONTROLLING THE STABILITY OF PROTEINS

CURRENT APPLICATION DATA:

APPLICATION DATA:

FILING DATE: 25-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                    Score 599.6; DB 7;
Pred. No. 8.2e-93;
); Mismatches 324;
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Best Local Similarity 71.0%;
Matches 861; Conservative (
                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1566
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APPLICANT: MRABET, NADIR:LASTERS, IGNACE;STANSSENS, PATRICK
MATHYSERS, GASTON;MODAK, SHOSHANA;QUAX, WILHELMUS J.
TITLE OF INTERPION: METHODS AND MEANS FOR CONTROLLING THE
STABILITY OF PROTEINS
NUMBER OF SEQUENCES: 22
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/398,706
FILING DATE: 25-AUG-1989
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Pred. No. 1.1e-92;
); Mismatches 302;
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Best Local Similarity 72.0%;
Matches 847; Conservative
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OTHER INFORMATION: /product= "xylose isomerase (glucose isomerase)"
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /standard_name= "D-xylose ketol isomerase"
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APPLICANT: QUAX, WILHELMUS
APPLICANT: LUTTEN, RUDOLF G.M.
APPLICANT: SCHUUTHUIZEN, PAUL W.
TITLE OF INVENTION: NOVEL GLUCOSE ISOMERASE ENZYMES ITILE OF INVENTION: THEIR USE
NUMBER OF SEGADUCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: MOITISON & FOOISTET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 598.4; DB 1;
Pred. No. 1.3e-92;
0; Mismatches 301;
                                                             coagetegecatggaccacetgetgggegeeeggg 1419
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ATTORNEY/AGENT INFORMATION:
NAME: Rate H. Murashige
REGISTRATION NUMBER: 29,959
REFERENCE/COKET NUBER: 24,959
REFERENCE/COKET NUBER: 24,959
TELEPHONE: (415) 327-7250
TELEFAX: (415) 327-2951
TELEFAX: 706141
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1182 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
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CITY: Menlo Park
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APPLICATION NUMBER: US/07/640,476
FILING DATE: 19910110
                                                                                                                                                                      Sequence 4, Application US/07640476
Patent No. 5376536
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic)
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ilarity 72.1%;
Conservative (
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LOCATION: 1..1182
IDENTIFICATION METHOD:
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ANTI-SENSE: N
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US-07-640-476-4
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ATGGCCGGGCTTAACTTTGTCCACGCCGTGGCCCAGGCTCTCGACGCCGGGAAGCTTTTC 1010
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TITLE OF INVENTION: AQUATICUS, XYLOSEISOMERASE AND PROCESS FOR PREPARATION OF THE OF INVENTION: FRUCTOSE
TOTALE OF INVENTION: FRUCTOSE
CORRESPONDENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSE: Burns, Doane, Swecker and Mathis
STREET: George Mason Bidg., Washington & Prince Sts.
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taccageceaececegaggacaggtteaectteggeetgtggacegteggetggeagggg 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC_Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/112,630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31.2%; Score 481.8; DB 1
62.5%; Pred. No. 3.8e-73;
                                                 PRICE AND DATA:
PRICE APPLICATION BAPA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/783,150
FILING DATE: 28-0CT-1991
ATTORNEY AGENT INFORMATION:
NAME: Rea, Teresa S.
REGISTRATION NUMBER: 30,427
REFERENCE/DOCKET NUMBER: 024705-007
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION S186-6620
ITELETAX: (703) 836-2021
TELETAX: 440 580
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1805 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                     Sequence 1, Application US/08112630 Patent No. 5411886 GENERAL INFORMATION:
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                                                                                                                                                                                                                       APPLICANT: UDAKA, Shigezo
APPLICANT: SAKAGCHI, Kenji
APPLICANT: YAMAGATA, Hideo
APPLICANT: DEKKER, Koen
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Matches 788; Conservative
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288..1448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY:
; LOCATION:
US-08-112-630-1
                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                     US-08-112-630-1
                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
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1491 AGCCCTGGTGCTGGACGAGGAGGGGTAGAAGCGCGCTGAGGCCCGGGCCCGGTACCCC 1550
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Pred. No. 3.6e-09;
0; Mismatches 694; Indels
                                                                                                                                                                                                                                                                                                                           COUNTRY: USA

ZIP: 20007-5109

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Ralease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,508
FILING DATE: 23-DEC 1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A:
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
RECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFEKK: 202 672 5399
                                                                                                      Sequence 7, Application US/08173508

PREENT NO. 5616485

GENERAL INFORMATION:
APPLICANT: Bartfeld, Daniel
APPLICANT: Batter, Michael J.
APPLICANT: Hadary, Dany
APPLICANT: Hadary, Dany
TITLE OF INVENTION: STREPTOMYCES PR.
TITLE OF INVENTION: STREPTOMYCES TRITILE OF INVENTION: STREPTOMYCES STREATION: CORRESPONDENCE SIS
CORRESPONDENCE ADDRESS:
ADDRESSE: FOLGY & Lardner
                                                                                                                                                                                                                                                                                         SEE: Foley & Lardner: 3000 K Street, N.W. Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: xxx TELEX: 904136
INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS: LENGTH: 1820 base pairs TYPE: nucleic acid
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Best Local Similarity 44.2%;
Matches 572; Conservative
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FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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FEATURE:
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LOCATION:
US-08-173-508-7
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US-08-173-508-7
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Best Local S
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603 CCCGCAGTGAACCCGTCGAGTGCCTGGACGGGCGCGGAGATGGACGCGTACACGCGCACCG
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APPLICANT: Garven, Phyllis
APPLICANT: Garven, Shelia
TITLE OF INVENTION: STREPTOMYCES PROTEASES AND IMPROVED
TITLE OF INVENTION: STREPTOMYCES STRAINS FOR EXPRESSION OF PEPTIDES AND
TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 21
            1440 gtacgcgcggtcgatctccctgcgtcgtcatgagggggtgctggggcggctcgaggcggcc 1499
                                    1716 GCTCGTAACCCCCCCCCCCCCCCCGGGACCCACGCCTCCGGGGCGGGGTTCGGAGCACC 1775
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: EN PC COMPATIBLE
CORPERATIONS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/265,310
FILING DATE: 24-JUN-1994
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/173,508
FILING DATE: 23-DEC-1993
ATTONNEY/AGENT INFORMATION:
NAME: BENTY, STEPPHEN A:
REGISTRATION NUMBER: 29,768
                                                                                            1776 CCGGGAAACTGTGTAGACTTGCCGACGTTGCTG 1808
                                                                   cggccccatcgtgctgcgtctcccgggggcgcgg 1532
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                                                                                                                                                                Sequence 7, Application US/08265310 Patent No. 5856166
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Butler, Michael J.
Hadary, Dany
Jenish, David
Krieger, Timothy
Malek, Lawrence T.
Soostmeyer, Gisela
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEFAX: 202 672 5399
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APPLICANT: Bartfe
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FEATURE:
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STREET: 30
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; LOCATION:
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                                                                       27;
   Length 1821;
Score 97; DB 3; Length 182
Pred. No. 6.6e-09;
0; Mismatches 625; Indels
   6.38;
44.88;
                                                                       Matches 529; Conservative
                                   Similarity
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1536 CCCGCGACCCGGCCCACCCCTACCGCTGGGCCGAGGCCCTCTCCGACCAGCTCACCTCCG 1595
                               1320 geacegegtaegagaettegaegtggaegeggeegeegegeatggeettegagege 1379
                                                          1596 GCCACCTCCTCACCTACGAGGGAGACGCCACACCGCGTACGGCCGCGGGAGCTCCTGCA 1655
                                                                                       APPLICANT: DeHOLF, Bradley S.
APPLICANT: DeHOLF, Bradley S.
APPLICANT: Kunstoss, Stuart A.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
AITLE OF INVENTION: POLYKETIDE SYNTHASE GENES NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSE: THOMAS G. PLANT 1501
STREET: LILLY CORPORATE CENTER
CITY: INDIANAPOLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: ASCI(DOS) Text only CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/08/804,227C FILING DATE: February 21, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: X-8231
TELEPHONE: 317-276-2459
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACIERISTICS:
                                                                                                                                                                                               Sequence 7, Application US/08804227C Patent No. 5876991 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM COMPALIDLE
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 44377 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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14046..20036
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31329..36071
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36155..41830
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20110..31284
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350..14002
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LOCATION:
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LOCATION:
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LOCATION:
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; LOCATION:
US-08-804-227C-7
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FEATURE:
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-08-804-227C-7
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Length 44377;

Query Match
5.5%; Score 85.2; DB 3; Length 4
Best Local Similarity 44.6%; Pred. No. 6.7e-07;
Matches 333; Conservative 0; Mismatches 413; Indels

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30604 CCGGCCGCGCTGCGCGCCACCGGAAGCGTCCCCGCCCTGCTGTCGGACCTCGTCGGGTCC 30663
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                                                      30004 GCCGCCCGCCGGGCCCCGGAGGCGCCGCGGAGGCTGGTCGCCGACCTCGCCGC 30063
                                                                                                                                                                                                                       30064 CTGGGCGCGTCGGCCACCGTGGTCGCCTGCGACGTCTCCGACGCGGACGCCGTCCGCGGA 30123
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791 ttcgccatcgagcccaagccgaacgagccgcgcgcggggacatcctgctgcccaccatcggc
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APPLICANT: Rulstoss, Stanrt A.
APPLICANT: Rao, Nagaraja R.
APPLICANT: Rao, Nagaraja R.
APPLICANT: Rao, Nagaraja R.
APPLICANT: Rao, Nark A.
APPLICANT: Roberck, Paul R., Jr.
TITLE OF INVENTION: PLATENOLIDE SYNTHA NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: PAUL R. CANTRELL 1138
STREET: LILLY CORPORATE CENTER
CITY: INDIANAPOLIS
STATE: IN
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Patent No. 5945320
GENERAL INFORMATION:
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30424 TCACTCGCCTGGGGTCTGTGTGCTCCGACACCGGATGGCACACGCACAGGAG 30483
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                                                                                                                                                                               30484 AGCCICCAGCGCGCTTCGCCCGCAGCGGCTTCCCGCCCTGTCCGCCACGCTGGGCGCC
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                                                                                                            1151 ggcgtgtggggcctccgcgggccgggtgcatgcgaactacctgatcctgaaggagcgcgcc
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Patent No. 5876923
GENERAL INFORMATION:
APPLICANT: Leopardi, Rosario
APPLICANT: Leopardi, Rosario
APPLICANT: Noizman, Bernard
TITLE OF INVENTION: HERPES SIMPLEX VIRUS ICP4 AS AN
TITLE OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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Pred. No. 1.6e-06;
0; Mismatches 622;
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COMPUTER: IBM PC COMPATLDS-0
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/690,473
FILING DATE: 26-UL-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30724 ACCGTCGGCGAGCCGCTCGCCGAGCG 30749
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NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: ARCD
TELECOMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEPHAX: 512/418-3000
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Best Local Similarity 43.6
Matches 497; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: P.O. Box 4433
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ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
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US-08-690-473-1
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US-08-690-473-1
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,198
FILING DATE:
                                                                                                                                                                                                                     US/08/804,198
                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CANTRELL, PAUL
REGISTRATION NUMBER: 36,470
REFERENCE/DOCKET NUMBER: P99113
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3885
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 44377 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 44.6%;
Matches 333; Conservative
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LOCATION:
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FEATURE:
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FEATURE:
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US-08-804-198-1
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361 cctcgacccggtcgacgtgcagcggctggccgaactgggcgcctacggagtgaccttcca
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ADDRESSEE: No. 59358370 No. 5935837d1sk of No. 5935837th America, Inc. STREET: 405 Lexington Avenue
CITY: New York
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                                                                       APPLICANT: Rasmussen, Micheal Dolberg
TITLE OF INVENTION: DNA CONStructs And Methods Of Producing
TITLE OF INVENTION: Xylose Isomerase
NUMBER OF SEQUENCES: 2
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Pred. No. 6.7e-06;
0; Mismatches 265; Indels
                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version : SOFTWARE: FastSEQ for Windows Version : CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/901,547A FILING DATE: 28-UUL-1997 CLASSIFICATION: 435 (TIORNEY APPROACH
                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Ellas J
RECISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4601.000-US
TELECOMUNICATION INFORMATION:
TELEPHONE: 212-667-0123
TELEFAX: 212-878-9655
               Sequence 1, Application US/08901547A Patent No. 5935837 GENERAL INFORMATION:
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MOLECULE TYPE: DNA (genomic)
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SEQUENCE CHARACTERISTICS:
LENGTH: 1668 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 47.3%;
Matches 238; Conservative
                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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101..1433
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JS-08-901-547A-1
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US-08-901-547A-1
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                                                                                                        12;
                                                                   Length 1908;
                                                                                                        Indels
                                                                   Score 78.6; DB 1;
Pred. No. 7.8e-06;
); Mismatches 639;
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                                                                    5.18;
                                                                                                          Conservative
263..1756
                                                                                     Similarity
; LOCATION:
US-08-173-508-1
                                                                          Local s.
504;
                                                                      Query Match
                                                                                         Best Loca
Matches
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                                                                      tcgccttcatcgagcgcctggagcgccccgagctgtacggtgtcaaccccgaggtgggcc
                                                                                                      852 ACGCTTTCCTGAAGAACCACGGCCTTGATGAGTACTTCAAGTTCAACATTGAAGCGAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/173,508
FILING DATE: 23-DEC-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Met at position -39
represents fMet"
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                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Bartfeld, Daniel
APPLICANT: Butler, Michael J.
APPLICANT: Butler, Michael J.
APPLICANT: Jenish, Dany
APPLICANT: Jenish, David
APPLICANT: Krieger, Timothy
TITLE OF INVENTION: STREPTOMYCES PR.
TITLE OF INVENTION: STREPTOMYCES ST.
TITLE OF INVENTION: POLYBEPTIDES
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                              978 agetettecacategaceteaae 1000
                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08173508
Patent No. 5616485
GENERAL INFORMATION:
                                                                                                                                                                                                                                                972 AACTIGGAAGCATCGACGCCAAC 994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: BENY, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 1874
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEPHONE: 202 672 5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29,768
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 904136
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1908 base pairs
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LOCATION: 146..148
OTHER INFORMATION: /not
OTHER INFORMATION: repi
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STRANDEDNESS: double
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ZIP: 20007-5109
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LOCATION:
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                                                                                                                                                                                                                                                               Length 1908;
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OTHER INFORMATION: /note= "Met at position -39 OTHER INFORMATION: represents fmet" FEATURE: NAME/KEY: sig_peptide LOCATION: 146..262 FEATURE:
                                                                                                                                                                                                                                                            Score 78.6; DB 3;
Pred. No. 7.8e-06;
0; Mismatches 639;
                                                                                                                                                                                                                                                            Query Match 5.1%;
Best Local Similarity 43.6%;
Matches 504; Conservative
                                                                                                                                            mat_peptide
263..1756
                                                                                                                                          ), NAME/KEY;
, LOCATION:
US-08-265-310-1
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APPLICANT: Butler, Michael J.
APPLICANT: Butler, Michael J.
APPLICANT: Hadary, Dany
APPLICANT: Hadary, Dany
APPLICANT: Krieger, Timothy
APPLICANT: Krieger, Timothy
APPLICANT: Malek, Lawrence T.
APPLICANT: Malek, Evanence T.
APPLICANT: Malexy, Eva
APPLICANT: Malexy, Eva
APPLICANT: Krygaman, Phyllis
APPLICANT: STREPTOMYCES PROTEASES AND IMPROVED
TITLE OF INVENTION: STREPTOMYCES STRAINS FOR EXPRESSION OF PEPTIDES AND
TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 21
  1251 gigoogoooggoiogaccagoiogacgagoocaacogogoogacggooigoaggoooigo 1310
                                                                                                             1281 CACCCGACCTGTCCGACACGGGGGAAGGCTCCGGGGAAAGGGGAAGGCGTCTACA 1340
                                                                                                                                                                                                              1341 CGGCCGTCGAGTGCACCGACGCCAAGTGGCCCGAACTGGCGCACCTGGGACCGGGACA 1400
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: BACENTIN Release #1.0, Version #1.25
SURREWT APPLICATION DATA:
APPLICATION NUMBER: US/08/265,310
FILING DATE: 24-UN-1994
CLASSIFICATION NUMBER: US 08/173,508
FILING APPLICATION DATA:
APPLICATION NUMBER: US 08/173,508
FILING APPLICATION STATE:
APPLICATION NUMBER: US 08/173,508
FILING DATE: 33-DEC-1993
ATTORNEY/ACENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 18740/133/CACO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5399
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08265310 Patent No. 5856166 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W. CITY: Washington, D.C. CITY: USA ZIP: 20007-5109
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INFORMATION FOR SEQ 1D NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1908 base pairs
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                            1371 togagogoctogaco 1385
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ADDRESSEE: Foley & LA
STREET: 3000 K Stree
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EDNESS: double
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LOCATION:
FEATURE:
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Patent No. 5821339

GENERAL INFORMATION:
APPLICANT: Schaffer, Priscilla A.
APPLICANT: Schaffer, Compositions and Methods for Treatment of Herpesvirus
TITLE OF INVENTION: Compositions and Methods for Treatment of Herpesvirus
TITLE OF INVENTION: Infections
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Macklewicz & No. 5821339ris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STREE: PA
                                                                                                                                               gigecgeceggetegaceagetegecgageceacegeggeegaeggeetgeaggeetge 1310
                                                                                                                                                                                                                              GGCTGAAGCTGCGCCGCCGCCGCGGAAGAAGCCGCTGGGCGGCGTCGTCGGACCGGCCG 1166
                             cgcggaccgaggacatcgacggcgtgtgggcctccgcggggccgggtgcatgcgcaactacc 1190
                                                       1167 AGCTGATCTCCTTCTTCCAGAGCGCCCCGTACTACGACTCCGCCTGGGCGCCCGACCGCGG 1226
                                                                                                                1227 AGATCTTCAGCAAGTACGTCGCCG-----GCGACACCCAGGCGCTCGTCGACGCCCCG 1280
                                                                                      tgatectgaaggagegegeegeetteegtgeegaeeeggaggteeaggaggeettge
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                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
RELECOMMUNICATION INFORMATION:
FELERHONE: (215) 568-3100
TELERAX: (215) 568-3100
TELERAX: (215) 568-3109
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 12001 base pairs
TYPE: nucleic acid
STRANDENNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: BM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/458,568A

FILING DATE: 02-JUNE-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION UNMBER: US 08/065,146

FILING DATE: 05-MAY-1993

CLASSIPICATION 1435

ATTORNEY/AGENT INFORMATION:

NAME: Leary Ph.D., Rathryn R.

REGISTRATION NUMBER: 36,317

PREFEDENCE ADOLOGYET MIMPRED: DETERMINED
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HYPOTHETICAL: NO
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                                                     Gaps
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                                                                                                                                                                                                                                                                   1620 ccerceacreccreccreccecesesarccresassesceresceasses
                                                                                                                                                                                                                                                                                                                                                                                                                                    498 acgegaceggeatgacegtteegatggeeaceaceaectetteaeceaecegtettea
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                                                                                                                                                                                                                                                                                                                            cettegggggggggcgtccgaccgagcgcgaggcgcacgtcaagcggttccgtcaggcgctcg
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  Length 12001;
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Score 78.6; DB 2;
Pred. No. 8.2e-06;
0; Mismatches 614;
  5.18;
  Query Match
Best Local Similarity 43.55
Matches 488; Conservative
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Search completed: March 22, 2000, 23:31:38 Job time: 1555 sec
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                                                                                                                                                                                            APPLICANT: Ryan, Michael J.
APPLICANT: Lotvin, Jason A.
APPLICANT: Lotvin, Jason A.
APPLICANT: Strathy, Nancy
APPLICANT: Strathy, Nancy
TITLE OF INVENTION: Cloning of the biosynthetic pathway for
TITLE OF INVENTION: useful therein
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4
7130 AGCTCGCCGCGTCAAGGACCTCGCCGAACGCTGGAACCGGCTCGCCGAGTTCGAGTTCG 7071
                    7250 AGGTCGCCGAGCGCCCCGGCGGCACCACCCTCACCCTCACCACGAGGTTCAGCGCGCTCG 7191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7190 ACGACGACCCGCAGGGCCTGCGCTGGATCAGCGAGGCGACGGACCGCAACAGCCGCAGCG 7131
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Pred. No. 1.3e-05;
0; Mismatches 581; Indels
                                                                                   3660 ececciaceaceacearaaceccaaceaceaceeccecee 3618
                                                         1377 gcctcgaccagctcgccatggaccacctgctggggcgcccgcgg 1419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/125,468
FILING DATE: 22-SEP-1993
CLASSIFICATION: 435
ATONNEY/AGENT INFORMATION:
NAME: TSEVEOS, Estelle J
REGISTRATION NUMBER: 31,255-02
TELECOMMULCATION INFORMATION:
TELEPHONE: (201)831-324
TELEPAX: (201)831-3305
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                             RESULT 15
US-08-125-468-1/c
; Sequence 1, Application US/08125468
; Patent No. 5589385
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ilarity 44.8%;
Conservative
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nucleic acid
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                            CITY: Wayne
STATE: New Jersey
COUNTRY: USA
ZIP: 07470
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Best Local Similarity
Matches 491; Conservat
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                                                                                                                                                                                    GENERAL INFORMATION:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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AL053013 Drosophil AL066051 Drosophil

Description

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Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr - Web : www.genoscope.cns.fr - Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
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melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw ap, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be location/Qualifiers
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Pteryota; Neoptera; Endopteryota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/db_rref="taxon:727"
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila
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DNA GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
AL053013.1 GI:4934461
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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- Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Marmoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Encoppila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
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melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the Isogenic strain v2: on bw, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/organism="Drosophila melanogaster"
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/clone_lib="RPCI-98"
/clone="BACR14N09"
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SOURCE ORGANISM

AUTHORS TITLE REFERENCE

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Drosophila melanogaster genome survey sequence TET3 end of BAC #BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/db_xref="taxon:7227"
/clone_lib="RECI-98"
/clone="BACR19D16"
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12.8%; Pred. No.
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Direct Submission

La Submitted (02-1018-1999) Genoscope - Centre National de Sequencage :

Submitted (02-1018-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr - Web : www.genoscope.cns.fr |

Web : www.genoscope.cns.fr |

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oscogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the Isogenic strain visc n A more detailed describtion of the library and how to order individual BAC clones, the entire library or fillers for hybridization from the BACPAC Resource Center can be found at http://Dacpac.med.buffalo.edu/drosophila_bac.htm.
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CNSOD6XK 935 bp DNA GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence T7 end of BAC #
BACR14N09 of RPCI-98 library from Drosophila melanogaster (fruit
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 935
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/db_xref-"taxon:7227"
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/clone="BACR14N09"
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Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
401 Queen Anne Avenue North, Seattle, WA 98109, USA
401 Cones Anne Avenue North, Seattle, WA 98109, USA
Frax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
gotgggcgcccgcgggctgaaccggggcgacgaggggtacgcggcggtcgatctccctgcgt 1464
                                                                                                                                                                                                                                                                                                                                                     AQ893581 1205 bp DNA GSS 10-NOV-1999 HS_4832_A2_C09_SP6E CIT Approved Human Genomic Sperm Library D sapiens genomic clone Plate=4832 Col=18 Row=E, genomic survey
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1 (bases 1 to 1205)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman,
                                                                                                                                                Hood,L.
Sequence-tagged connectors: A sequence approach to mapping
                                                                                                          1046 Geegeegeegeccccssssssegsscccsccccesscccssseccescccsses
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Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
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Plate: 4832 row: E column: 18
Seg primer: T7
Class: BAC ends
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Pred. No. 0.13;
0; Mismatches 487;
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/clone="Plate=4832 Col=18 Row=E"
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Location/Qualifiers
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AQ893581.1 GI:6349771
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Conservative
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pbelobacil.
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 1285 cgcggccgacggcctgcaggccctgctggccgaccgcaccgcgtacgaggacttcgacgt 1344
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Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta,
Pteryota, Neoptera, Endopterygota, Diptera, Brachycera,
Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
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84; Mismatches 219; Indels
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/plasmid="pBeloBAC11"
/db_xrefe="baxon:7227"
/clone_lib="DrosBAC"
/clone="BACN15E10"
/note="end: T7"
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of DrosBAC library fr
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Determination of this BAC-end sequence was carried out as part of a collaboration of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
Submitted (23-JUL-1999) Genoscope – Centre National de Sequencage
BP 191 91006 EVRY cedex – FRANCE (E-mail : segrefégenoscope.cns.fr
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Drosophila melanogaster genome survey sequence T7 end of BAC #
BACR14B09 of RPCI-98 library from Drosophila melanogaster (fruit
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
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Best Local Similarity 33.1%; Pred. No. 0.24;
Matches 151; Conservative 85; Mismatches 220; Indels
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1. 1203
/ Organisa-"Drosophila melanogaster"
/ plasmid="pBeloBAC11"
/ db_xref="taxon.7227"
/ clone="lb-"lorosBAC"
/ clone="BACN15E10"
/ note="end : T7"
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Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etded du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Pteryyota; Neoptera; Endopterygota; Ditera; Brachycera;
Muscomorpha; Ebhydroidea; Drosophilldae; Drosophila.
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                                                                                                                          Jurect submissions

Submitted (02-JUN 1999) Genoscope - Centre National de Sequencage:
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
- Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACS. For further information please see http://www.fruifly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the Isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
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/db_xref="taxon:9606"
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDCP) - thtp://www.edcp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre Fitted of Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segrefégenoscope.cns.fr
                                                                                                            CNSOLOEW 1009 bp DNA GSS 26-JUL-1999
Drosophila melanogaster genome survey sequence SP6 end of BAC
ARACNOSP19 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilldae; Drosophila.
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1. .1009
/organism="Drosophila melanogaster"
/plasmid="pBeloBAcil"
/db_xref="taxon:7227"
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Best Local Similarity 30.4%; Pred. No. 0.62;
Matches 109; Conservative 87; Mismatches 162;
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/clone="BACN03P19"
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Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Library avallability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
Plate: 963 row: J column: 13
Seq Primer: 876
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AQ743419 1054 bp DNA GSS 16-JUL-1999 HS_5387_B1_E07_SP6 RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=963 Col=13 Row=J, genomic survey sequence.
                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1054)
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/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
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Best Local Similarity 48.0%; Pred. No. 0.81;
Matches 242; Conservative 0; Mismatches 257;
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High Throughput Sequencing Center
Wigh Throughput Sequencing Center
Wigh Throughput Sequencing Center
Windership of Washington
Tol. (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
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                                                               ctccctgcgtcgtcatgagggggtgctggggcggctcgaggccgggcccgatcgtgct 1514
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 965)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.)
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/db_xref="taxon:9606"
/clone="Plate=4832 Col=8
/clone_lib="CIT Approved
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Matches 332; Conservative
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
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1 (bases 1 to 753)

Ming,R.A. and Dean,R.A.

A BAC End Sequencing Framework to Sequence the Rice Genome Unpublished (1998)
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Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                       RESULT 15
CNS0052P/c
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TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
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//Clone="habd0044095"
//Clone="habd0044095"
//Clone="habb0044095"
//Lissue_type="Leaf"
//Lab_host="E.coli DH10B"
//Lab_host="E.
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4.0%; Score 61.2; DB 88; Length 753;
Best Local Similarity 45.8%; Pred. No. 1.6;
Matches 247; Conservative 0; Mismatches 289; Indels 3.
                                                                                                                                                                     /organism="Oryza sativa"
Seg primer: TAATACGACTCACTATAGGG
Class: BAC ends
High quality sequence stop: 395.
Location/Qualifiers
                                                                                                                                                                                                    /strain="Japonica"
/cultivar="Nipponbare"
/db_xref="taxon:4530"
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Jurect Submission of the Samuel Sequencage: Submisted (02-JUN-1999) Genoscope - Centre National de Sequencage: BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr - Web: www.genoscope.cns.fr)

- Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruilily.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcorI digestion of Insophila Day the SDGP from the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_Dac.htm.
                                                                                                                                                                                                                                              CNS0052P 844 bp DNA GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR11P16 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1209 ccgccgccttccgtgccgacccggaggtccaggaggccctgcgtgccggcccggctcgacc 1268
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634 CBYBCNTSCSYYSYSBCSGCSSSSSSSSSSBYSCCCBCCCBGYCGCYSBVCSSBST 575
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/db_xxef="Laxon:7227"
/clone_lb="RPCI-98"
/clone="BACR11P16"
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4.0%; Score 61.2; DB 79;
Best Local Similarity 18.6%; Pred. No. 1.7;
Matches 51; Conservative 128; Mismatches 95;
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Thu Mar 23 09:16:06 2000

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Search completed: March 22, 2000, 23:16:27 Job time: 724 sec

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Sequence 3
Sequence 2
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GENERAL INFORMATION:
APPLICANT: Lasters, Ignace
APPLICANT: Lasters, Ignace
APPLICANT: Quax, Wilhemus J.
APPLICANT: Quax, Wilhemus J.
APPLICANT: Van Der Laan, Jan M.
TITLE OF INVENTION: NOVEL GLUCOSE ISOMERASES HAVING
TITLE OF INVENTION: MATERED SUBSTRATE SPECIFICITY
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: SAFET: Addlefield Road, Suite 200
CITY: Menlo Park
STATE: California
COUNTY: USA Middlefield Road, Suite 200
CITY: Menlo Park
STATE: California
COMPUTER: Lam PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O7/637,870
FILING DATE: 19910104
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29,959
TELECHOME: TELECHONE: TELECHO
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92.8%; Pred. No. 2.7e-182;
iive 14; Mismatches 12;
US-08-901-547A-2
US-07-637-817-99-6
US-07-637-399-6
US-08-112-703-6
US-07-637-870-7
US-07-637-870-7
US-07-637-870-8
US-07-637-899-5
US-07-637-399-5
US-07-637-399-5
US-08-606-112-703-5
US-08-606-113-703-5
US-08-606-1143-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
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; Patent No. 5310665
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TELEX: 706141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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         STRANDEDNESS: single
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US-07-637-870-4
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Best Local Similarity
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239.853 Million cell updates/sec
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Sequence 7, Appli
Sequence 7, Appli
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Sequence 9, Al
Sequence 12, A
Sequence 9, Al
Sequence 8, Al
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Sequence 6, 2
Sequence 6, 2
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Sequence 2,
Sequence 2,
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                                                                                                                                                                                                                       March 22, 2000, 23:30:54; Search time 21.4 Seconds
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1: /cgn2_6/ptodata/1/laa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/laa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/laa/6_COMB.pep:*
4: /cgn2_6/ptodata/1/laa/PCTUS9_COMB.pep:*
5: /cgn2_6/ptodata/1/laa/PCTUS9_COMB.pep:*
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US-07-640-476-11

US-07-637-399-9

US-07-640-476-12

US-07-640-476-12

US-07-640-476-12

US-07-637-399-8

US-07-640-476-10

US-07-640-476-10

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US-07-640-476-10
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US-07-637-399-1
US-08-112-703-1
US-07-640-476-5
                                       GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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US-07-637-399-3
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Listing first 45 summaries
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Maximum DB seq length: 1000000
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1900 1900 1900 1892.5 1859 1859 1859 1859

Score

Result No.

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Database

Searched:

Perfect score:

Sequence:

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Run on:

Scoring table:

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Sequence 7, Application US/07637399;
Patent No. 5340738;
GENERAL INFORMATION:
APPLICANT: Lambeir, Anne-Marie
APPLICANT: Lasters, Ignace
APPLICANT: Marser, Nance
APPLICANT: Wan Der Laan, Jan M.
APPLICANT: Wan Der Laan, Jan M.
APPLICANT: Wilhelmus J.
APPLICANT: Wilhelmus J.
APPLICANT: Wilhelmus J.
APPLICANT: Wan Der Laan, Jan M.
APPLICANT: Misser, Onno
TITLE OF INVENTION: ALTERED PH OPTIMUM
TITLE OF INVENTION: ALTERED PH OPTIMUM
TITLE OF INVENTION: ALTERED PH OPTIMUM
TITLE STAURESS:
ADDRESSEE: MORTISON & FOGESTER
STREET: 545 MIDDLESS:
ADDRESSEET: MORTISON & FOGESTER
CITY: Menio Park
STREE: California
COUNTY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION NUMBER: US/07/637,399
FILLIG DATE: 19910104
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                             NAME: MILEBAIGE, Kale H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 461
TELECOMMUNICATION:
TELEPHONE: 415-327-7250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 415-327-2951
TELEX: 706141
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
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US-07-637-399-7
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                                                                                                                                                                                61 FGSSDTERESHIKRFRQALDATGMIVPMATINLFTHPVFKDGGFTANDRDVRRYALRKII 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: OUAX, WILHELMUS
APPLICANT: UNITED, RUDOLE G.M.
APPLICANT: SCHUURHUIZEN, PAUL W.
APPLICANT: SCHUURHUIZEN, PAUL W.
APPLICANT: MRABET, NADIR W.
APPLICANT: MADIR USE
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: MATTISON & FOOTSTET
STREET: 545 MIddlefield Road, Suite 200
CITY: Menlo Park
STATE: CA
    Length 388;
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93.6%; Score 1900; DB 1; 92.8%; Pred. No. 2.7e-182; ive 14; Mismatches 12;
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APPLICATION NUMBER: US/07/640,476
FILING DATE: 19910110
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY AGENT INFORMATION:
NAME: Kate H. Murashige
REGISTATION UNDHER: 29,959
REPERENCE/DOCKET NUMBER: 2461
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 327-7250
TELEFAX: (415) 327-7251
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 7, Application US/07640476; Patent No. 5376536
                                         Conservative
                    Similarity
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                    Best Local Sim
Matches 360;
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US-07-640-476-7
  Query Match
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                                                                                  Length 388;
                                                                                                               Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                 93.6%; Score 1900; DB 1;
92.8%; Pred. No. 2.7e-182;
tive 14; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lambeir, Anne-Marie
APPLICANT: Lasters, Ignace
APPLICANT: Mrabet, Nadir
APPLICANT: Quax, Wilhelmus J.
APPLICANT: Van Der Laan, Jan M.
APPLICANT: Willer, Onno TITLE OF INVENTION: ALTERED PH OPTIMUM
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STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/08112703
Patent No. 5384257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29,959
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NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-AUG-1993
                                                                                 Query Match 93.6
Best Local Similarity 92.8
Matches 360; Conservative
         ; TOPOLOGY: linear; MOLECULE TYPE: protein US-07-640-476-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
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AMINO ACID
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CLASSIFICATION:
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120 RNIDLAVELGAKVYVAWGGREGAESGAAKDVRAALDRMKEAFDLLGEYVTSQGYDIRFAI 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             300 ASAAGCMRNYLILKERAAAFRADPEVQEALRAARLDQLAEPTAADGLQALLADRTAYEDF 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 FGASDIEREAHVKRFRQALDAIGMIVPMATINLFTHPVFKAGAFTANDRAVRRYALRKII 119
                                                                                                                                                                                                                                                                                                                                                                                                   1 MNYQPTPEDRFTFGLWTVGWQGRDPFGDATRPALDPVD-VQRLAELGAYGVTFHDDDLIP
                                                                                                                                                                                                                                                                                        Length 388;
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Patent No. 5376536
CENERAL INFORMATION:
APPLICANT: QUAX, WILHELMUS
APPLICANT: LUTTEN, RUDOLF G.M.
APPLICANT: SCHUUHUIZEN, PAUL W.
APPLICANT: MARBET, NADIR
TITLE OF INVENTION: NOVEL GLUCOSE ISOMERASE ENZYMES AND TITLE OF INVENTION: THEIR USE
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                   93.6%; Score 1900; DB 1; 92.8%; Pred. No. 2.7e-182; iive 14; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Morrison & Foerster
STREET: 545 Middlefield Road, Suite
CITY: Menlo Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     360 DVD-AAARGMAFERLDQLAMDHLLGARG 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DVDAAAARGMAFEHLDQLAMDHLLGARG 388
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APPLICATION NUMBER: US/07/640,476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                     TELEFAX: 415-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 anino acids
TYPE: amino acid
STRANDEDNESS: single
1 TOPOLOGY: linear
relecommunication information:
   Telephone: 415-813-5600
   Telefax: 415-494-0792
                                                                                                                                                                                                                                                                                   Query Match 93.6
Best Local Similarity 92.8
Matches 360; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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ZIP: 940:
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RESULT 7
US-07-637-399-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180 EPKPNEPRGDILLPTIGHALAFIERLERPELYGVNPEVGHEQMAGLNFPHGIAQALWAGK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LFHIDLNGQSGIKYDQDLRFGAGDLRAAFWLVDLLESAGWEGPRHFDFKPPRTEDIDGVW 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   300 ASAAGGMRNYLILKERAAAFRADPEVQEALRAARLDQLAEPTAADGLQALLADRTAYEDF 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 FGASDTEREAHVKRFRQALDATGMTVPMATTNLFTHPVFKAGAFTANDRAVRRYALRKTI 119
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FILING DATE: 1991ULLU
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RATE H. MURABING
REGISTRATION NUMBER: 29,559
REFERENCE/DOCKET NUMBER: 24615-20009.20
TELEPHONE: (415) 327-7250
TELEFAX: (415) 327-7251
TELERX: 706141
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 389 amino acids
TYPE: AMINO ACID
STRANDEDNESS: SINGLE
"OFFICE HORSES: SINGLE
"OFFICE HORSES: SINGLE
"OFFICE HORSES: SINGLE
                                                                                                                                                                                                                                                                                        HYPOTHETICAL: NO ORIGINAL SOURCE: ORIGINAL SOURCE: ORGANISM: Streptomyces violaceoniger STRAIN: CBS 409.73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 360 DVDAAARGMA--FERLDQLAMDHLLGARG 386
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Patent No. 5310665
GENERAL INFORMATION:
APPLICANT: Lembler, Anne-Marle
APPLICANT: Lasters, Ignace
                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Protein
LOCATION: 1.389
PUBLICATION INFORMATION:
AUTHORS: TITRABY,
JOURNAL: Nucleic Acids Res.
                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                     VOLUME: 16
PAGES: 9337-
DATE: 1988
US-07-640-476-11
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-07-637-870-3
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60 FGASDTEREAHVKRFRQALDATGMTVPMATTNLFTHPVFKAGAFTANDRAVRRYALRKTI 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 RNIDLAVELGASVYVAWGGREGAESGAAKDVRDALDRMKEAFDLLGEYVTEQGYDLKFAI 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MNYQPTPEDRFTFGLWTVGWQGRDPFGDATRQALDPAESVRRLSELGAYGVTFHDDDLIP 60
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91.6%; Score 1859; DB 1; Length 387;
Best Local Similarity 91.2%; Pred. No. 3.4e-178;
Matches 353; Conservative 15; Mismatches 17; Indels
APPLICANT: Quax, Wilhemus J.
APPLICANT: Van Der Laan, Jan M.
TITLE OF INVENTION: NOVEL GLUCOSE ISOMERASES HAVING
TITLE OF INVENTION: ALTERED SUBSTRATE SPECIFICITY
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                              COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARRE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/637,870
FILING DATE: 19910104
                                                                                                                                                            ADDRESSEE: Morrison & Poerster
STREET: 545 Middlefield Road, Suite 200
CITY: Menlo Park
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: MURShige, Kate H.
REGISTRATION NUMBER: 29,959
RESERENCE/DOCKET NUMBER: 24615-20019.00
TELECOMMUNICATION INFORMATION:
TELEPRA: 415-813-500
TELEFAX: 415-827-2951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   360 DVD-AAARGMAFERLDQLAMDHLLGAR 385
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INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 387 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: AMINO ACID
STRANDEDNESS: S1r
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US-07-637-870-3
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120 RNIDLAVELGAKVYVAWGGREGAESGAAKDVRAALDRMKEAFDLLGEYVTSQGYDIRFAI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 FGASDTEREAHVKRFRQALDATGMTVPMATTNLFTHPVFKAGAFTANDRAVRRYALRKTI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MNYQPTPEDRFTFGLWTVGWQGRDPFGDATRPALDPVD-VQRLAELGAYGVTFHDDDLIP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 12, Application US/07640476
Patent No. 5376536
GENERAL INFORMATION:
APPLICANT: QUAX, WILHELMUS
APPLICANT: LUITEN, RUDOLF G.M.
APPLICANT: SCHUURHUIZEN, PAUL W.
APPLICANT: MAABET, NADIR
TITLE OF INVENTION: THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91.6%; Score 1859; DB 1; 91.2%; Pred. No. 3.4e-178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: Kate H. Murashige
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 24615-20009.20
RELEPHONE: (415) 327-2951
TELEPHONE: (415) 327-2951
TELERAX: (415) 327-2951
TELERAX: (415) 327-2951
TELERAX: (415) 327-2951
SEQUENCE CHARACTERISTICS:
LENGTH: 387 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                        3: Morrison & Foerster
545 Middlefield Road, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptomyces violaceoruber
                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/640,476
FILING DATE: 19910110
CLASSIFICATION: 435
360 DVD-AAARGMAFERLDQLAMDHLLGAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 387 amino acids
AMINO ACID
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Matches 353; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ), NAME/KEY: Protein
), LOCATION: 1..387
US-07-640-476-12
                                                                                                                                                                                                                                                                                                                                                                                         STREET: 545 Midus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94025
                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                   RESULT 8
US-07-640-476-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 FGASDTEREAHVKRFRQALDATGMTVPMATTNLFTHPVFKAGAFTANDRAVRRYALRKTI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 RNIDLAVELGAKVYVAWGGREGAESGAAKDVRAALDRMKEAFDLLGEYVTSQGYDIRFAI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EPKPNEPRGDILLPTIGHALAFIERLERPELYGVNPEVGHEQMAGLNFPHGIAQALWAGK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LFHIDLNGQSGIKYDQDLRFGAGDLRAAFWLVDLLESAGWEGPRHFDFKPPRTEDIDGVW 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 LEHIDLNGQSGIKYDQDLRFGAGDLRAAFWLVDLLERAGYAGPRHFDFKPPRTEDFDGVW 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASAAGCMRNYLILKERAAAFRADPEVQEALRAARLDQLAEPTAADGLQALLADRTAYEDF 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
               GENERAL INFORMATION:
APPLICANT: Lasters, Ignace
APPLICANT: Lasters, Ignace
APPLICANT: Marbet, Madir
APPLICANT: Quax, Wilhelmus J.
APPLICANT: Van Der Laan, Jan M.
APPLICANT: Wasset, Onno
TITLE OF INVENTION: NOVEL GLUCOSE ISOMERASES WITH AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
DEPLICATION NUMBER: US/07/637,399
FILING DATE: 19910104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
91.6%; Score 1859; DB 1;
Best Local Similarity 91.2%; Pred. No. 3.4e-178;
Matches 353; Conservative 15; Mismatches 17;
                                                                                                                                                                                                                 ...ure:SSEE: __ nuuress:
STREET: 545 Middleffeld Road, Suite 200
CITY: Menlo Park
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 4615-0020.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-327-7250
TELEPHONE: 415-327-2951
Sequence 9, Application US/07637399
                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OOPERATING SYSTEM: PC-DOS/MC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 415-327-2951
TELEX: 706141
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 387 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison
                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
US-07-637-399-9
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CLASSIFICATION:
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LFHIDLNGOSGIKYDODLRFGAGDLRAAFWLVDLLESAGWEGPRHFDFKPPRTEDIDGVW 299
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                                                                                                                                                                                                                                                                                                         FGSSDTERESHIKRFRQALDATGMKVPMATTNLFTHPVFKDGAFTANDRDVRRYALRKTI 120
                                                         RNIDLAVELGAKVYVAWGGREGAESGAAKDVRAALDRMKEAFDLLGEYVTSQGYDIRFAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1734.5; DB 1; Length 348; Pred. No. 8.4e-166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Application US/07637399;
Patent No. 5340738;
GENERAL INFORMATION:
APPLICANT: Lambelt, Anne-Marie
APPLICANT: Lambelt, Andir
APPLICANT: Quax, Ignace
APPLICANT: Quax, Hilbelmus J.
APPLICANT: Van Der Laan, Jan M.
APPLICANT: Wan Der Laan, Jan M.
APPLICANT: Wan Set, Onno
ITILE OF INVENTION: NOVEL GLUCOSE ISOMERASES WITH AN TITLE OF INVENTION: ALTERED PH OPTIMUM
ITILE OF INVENTION: ALTERED PH OPTIMUM
ADDRESSEDEE: MOILISON & FOEISTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ā
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/637,399
FILING DATE: 19910104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Morrison & Foerster
STREET: 545 Middlefield Road, Suite 200
CITY: Menlo Park
STATE: California
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                              DVD-AAARGMAFERLDQLAMDHLLGAR 385
                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY, AGENT INFORMATION:
NAME: MUTASHIGG, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 4615
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-327-7250
TELEPAX: 415-327-7250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IBM PC compatible
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94.0%;
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INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: AMINO ACID
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Best Local Similarity
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US-07-637-399-8
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300 ASAAGCMRNYLILKERAAAFRADPEVQEALRAARLDQLAEPTAADGLQALLADRTAYEDF 359
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                                                                          LFHIDLNGQSGIKYDQDLRFGAGDLRAAFWLVDLLESAGWEGPRHFDFKPPRTEDIDGVW 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MNYQPTPEDRFTFGLWIVGWQCRDPFGDAIRQALDPAESVRRLSELGAYGVIFHDDDLIP 60
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                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Leaders, Anne-Marie
APPLICANT: Leaters, Ignace
APPLICANT: Leaters, Ignace
APPLICANT: Mrabet, Nadir
APPLICANT: Warbet, Nadir
APPLICANT: Wan Der Laan, Jan M.
APPLICANT: Wan Der Laan, Jan M.
APPLICANT: Wanset, Onno E. GLOCOSE ISOMERASES WITH AN TITLE OF INVENTION: MALTERED PH OPTIMUM
NUMBER OF SEQUENCES:
ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: EMP COMPUTER:
COMPUTER: TEM PC COMPUTER:
COMPUTER: PATENTIAL
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIAL Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/112,703
FILING DATE: 26-AUG.1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91.6%; Score 1859; DB 1;
91.2%; Pred. No. 3.4e-178;
ive 15; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4615002001
                                                                                                                                                                                                                              360 DVD-AAARGMAFERLDQLAMDHLLGAR 385
                                                                                                                                                                                                                                                    361 DVDAAAARGMAFEHLDQLAMDHLLGAR 387
                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/08112703 Patent No. 5384257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTONNEY AGENT INFORMATION:
NAME: Mureshige, Kate H.
REGISTRATION NUMBER: 29,959
REFRENCE/DOCKET NUMBER: 4615
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
TELEFAX: 415-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELERA: 415-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
LENGTH: 387 anino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 91.23
Matches 353; Conservative
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STRANDEDNESS: sir
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US-08-112-703-9
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STATE: CA
COUNTRY:
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US-08-112-703-9
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COMPUTER:
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US-07-637-870-5
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                                                                                                            61 FGASEAEREAHVKRFRQALDATGMTVPMATTNLFTHPVFKDGAFTANDRDVRXALRKTI 120
                                                                                                                                                                         240 LFHIDLNGOSGIKYDQDLRFGAGDLRAAFWLVDLLESAGWEGPRHFDFKPPRTEDIDGVW 299
                                                                                                                                                                                                                                                                                                    1 MNYQPTPEDRFTFGLWTVGWQGRDPFGDATRPALDPV-DVQRLAELGAYGVTFHDDDLIP 59
                                                RNIDLAVELGAKVYVAWGGREGAESGAAKDVRAALDRMKEAFDLLGEYVTSQGYDIRFAI
                                                                                                                                                                                                                      EPKPNEPRGDILLPTIGHALAFIERLERPELYGVNPEVGHEQMAGLNFPHGIAQALWAGK
                                                                                                                                                                                                                                                                                                                                                                 300 ASAAGCMRNYLILKERAAAFRADPEVQEALRAARLDQLAEPTAADGLQ 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/112,703
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Lasters, Ignace
APPLICANT: Mrabet, Nadir
APPLICANT: Quax, Wilhelmus J.
APPLICANT: Quax, Wilhelmus J.
APPLICANT: Van Der Laan, Jan M.
APPLICANT: Misset, Onno
TITLE OF INVENTION: NOVEL GLUCOSE ISOMER!
TITLE OF INVENTION: ALTERED PH OPTIMUM
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    олыЕR: US/08/112,703
26-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Morrison & Foerster STREET: 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/08112703
Patent No. 5384257
GENERAL INFORMATION:
APPLICANT: Lambeir, Anne-Marie
APPLICANT: Lasters, Ignace
APPLICANT: Mrabet, Nadir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFRENCE/DOCKET NUMBER: 4615
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELERAX: 415-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
TYPE: amino acid
STRANDEDNESS: single
;
TOPOLOGY: linear
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Palo Alto
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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Matches
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60 FGASDTEREAHVKRFRQALDATGMTVPMATINLFTHPVFKAGAFTANDRAVRRYALRKTI 119
                                                                                                                                                                                                          RNIDLAVELGAKVYVAWGGREGAESGAAKDVRAALDRWKEAFDLLGEYVTSQGYDIRFAI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                           LFHIDLNGQSGIKYDQDLRFGAGDLRAAFWLVDLLESAGWEGPRHFDFKPPRTEDIDGVW 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                    1 MNYQPTPEDRFTFGLWTVGWQGRDPFGDATRPALDPV-DVQRLAELGAYGVTFHDDDLIP 59
                                                                                                                                                                                                                                                                                                                                                                                           EPKPNEPRGDILLPTIGHALAFIERLERPELYGVNPEVGHEQMAGLNFPHGIAQALWAGK
Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             300 ASAAGCMRNYLILKERAAAFRADPEVQEALRAARLDQLAEPTAADGLQ 347
                                               Indels
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APPLICANT: Lasters, Ignace
APPLICANT: Lasters, Ignace
APPLICANT: Quax, Wilhemus J.
APPLICANT: Quax, Wilhemus J.
APPLICANT: Quax, Wilhemus J.
APPLICANT: Won Der Laan, Jan M.
TITLE OF INVENTION: NOVEL GLUCOSE ISOMERASES HAVING
TITLE OF INVENTION: ALTERED SUBSTRATE SPECIFICITY
NUMBER OF SECUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: Morrison & Foerster
STREET: SAS Middlefield Road, Suite 200
CITY: Menlo Park
  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/637,870
FILING DATE: 19910104
85.5%; Score 1734.5; DB 1
94.0%; Pred. No. 8.4e-166;
tive 13; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24615-20019.00
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/07637870 Patent No. 5310665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 19910104
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NÜMBER: 29,959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
TELEFAX: 415-327-2951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 347 amino acids TYPE: AMINO ACID
                                               Matches 327; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 706141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: California
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Query Match
Best Local Similarity
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ZIP: 94025
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US-07-637-870-2
                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                    EPKPNEPRGDILLPTIGHALAFIERLERPELYGVNPEVGHEQMAGLNFPHGIAQALWAGK 239
                                                                                                                                                                                                                                                                                                           60 FGASDTEREAHVKRFRQALDATGMTVPMATTNLFTHPVFKAGAFTANDRAVRRYALRKTI 119
                                                                                                                                                                                                                                                                                            240 LFHIDLNGQSGIKYDQDLRFGAGDLRAAFWLVDLLESAGWEGPRHFDFKPPRTEDIDGVW 299
                                                         1 MNYQPTPEDRFTFGLWTVGWQGRDPFGDATRPALDPV-DVQRLAELGAYGVTFHDDDLIP 59
                                                                        Gaps
                              ı,
 DB 1; Length 347;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 10, Application US/07640476

Sequence 10, Application US/07640476

GENERAL INFORMATION:
APPLICANT: LUITEN, RUDOLF G.M.
APPLICANT: LUITEN, RUDOLF G.M.
APPLICANT: MAMBET, NADIR
TITLE OF INVENTION: THEIR USE
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mortison & Foetster
STREET: 545 Middlefield Road, Suite 200
CITY: Meallo Park
STREET: CA
                            Indels
                                                                                                                                                                                                                                                                                                                                                    300 ASAAGCMRNYLILKERAAAFRADPEVQEALRAARLDQLAEPTAADGL 346
                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE:
85.2%; Score 1729.5; DB 1; 93.9%; Pred. No. 2.7e-165; ive 13; Mismatches 7;
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APPLICATION NUMBER: US/07/640,476
FILING DATE: 19910110
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KALEH H MLURBR: 24615-20009
REGISTRATION NUMBER: 24615-20009
REFERENCE/DOCKET NUMBER: 24615-20009
TELEPHONE: (415) 327-250
TELEPHONE: (415) 327-251
TELEFAX: 766141
INFORMATION FOR SEO ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 347 mnino acids
TYPE: AMINO ACID
TOPOLOGY: 11near
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 Query Match
Best Local Similarity 93.9
Matches 326; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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EPKPNEPRGDILLPTIGHALAFIERLERPELYGVNPEVGHEQMAGLNFPHGIAQALWAGK 239
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                                                                                                                                                                                                                                                                                    Query Match 85.2%; Score 1729.5; DB 1; Length 347; Best Local Similarity 93.9%; Pred. No. 2.7e-165; Matches 326; Conservative 13; Mismatches 7; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             300 ASAAGCMRNYLILKERAAAFRADPEVQEALRAARLDQLAEPTAADGL 346
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this protein is not complete."
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APPLICANT: Lasters, Ignace
APPLICANT: Quax, Wilhemus J.
APPLICANT: Van Der Lean, Jan M.
TITLE OF INVENTION: NOVEL GLUCOSE ISOMERASES HAVING
TITLE OF INVENTION: ALTERED SUBSTRATE SPECIFICITY
CORRESPONDENCE: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
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STREET: 545 Middlefield Road, Suite 200
CITY: Menlo Park
STATE: California
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                                                 Streptomyces thermovulgaris
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APPLICATION NUMBER: US/07/637,870
FILING DATE: 19910104
CLASSIFICATION: 435
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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; Patent No. 5310665
; GENERAL INFORMATION:
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NAME: MILASHIGG, Kate H.
REGISTRATION NUMBER: 29,959
MOLECULE TYPE: protein ORIGINAL SOURCE: ORGANISM: Streptomyce STRAIN: DSM 40444
                                                                                                                                          CCATION: 1..347
CTHER INFORMATION:
CTHER INFORMATION:
US-07-640-476-10
                                                                                                                      NAME/KEY: Protein
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                                                                                                                                                                                                                        6
                                                                                                                                                                                         Length 394;
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APPLICANT: Lasters, Ignace
APPLICANT: Mrabet, Nadir
APPLICANT: Mrabet, Nadir
APPLICANT: Mrabet, Nadir
APPLICANT: Wan Der Laan, Jan M.
APPLICANT: Wan Der Laan, Jan M.
APPLICANT: Waset, Onno
TITLE OF INVENTION: ALTERED PH OPTIMUM
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                           66.7%; Score 1353.5; DB 1
66.0%; Pred. No. 1.4e-127;
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STREET: 545 Middlefield Road, Suite 200
CITY: Menlo Park
STATE: Callfornia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
TELEFAX: 415-327-2951
TELEX: 706141
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTER.STICS:
LENGTH: 394 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
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Patent No. 5340738
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MEDIUM TYPE: Floppy
                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                ; TOPOLOGY: linear
US-07-637-870-2
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60 FGASDTEREAHVKRFRQALDATGMTVPMATTNLFTHPVFKAGAFTANDRAVRYALRKTI 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 394;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                   66.7%; Score 1353.5; DB 1;
66.0%; Pred. No. 1.4e-127;
iive 46; Mismatches 79;
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US/07/637,399
             FILING DATE: 19910104
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: MLASAIGE, Kate H:
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 4615
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION OF 327-2951
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 394 antho acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 66.0
Matches 260; Conservative
                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
APPLICATION NUMBER:
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US-07-637-399-2
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RESULT 1
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
                             OM nucleic - nucleic search, using sw model
                                                                                                       IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
               em_htg1:*
em_htg2:*
em_htg3:*
em_htg3:*
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gb_htg7:*

		Description	5518 Strep	AFI/0008 Streptomy M73789 Streptomyce	S.violaceo	Streptom	S73809 xylose isom	Streptomyc	Sequence 1	E01992 DNA sequenc	M15050 Actinoplane	AUG4UG NUCLEOLIGE	Nucleotide	A10241 A.missourie	X59466 Arthrobacte	D90256 T.thermophi	ა რ		2 2	St	Sec		20 0	0 Sequence	10	4 Streptom	50	و م	1 Streptomy	X8/246 Pseudorable	1 1	302 Streptom	S.S.	90 S.pri	339 Strep	541 Stre	215	13605 Str	57 Strepto	F04771
SUMMARIES		QI	SPY1	E S	. 7	SVXYL	573809	E15670	109223	E01992	AMSXYLI	A00400	A06404	A10241	ASXYLA	TTHXYLA	TIII/43	20020	SC7H2	STMSLPD	138962	SCH5		5 5	AC007500		AP000550	_	- 7	PVULSUS	CHMEDG	AF058302	SPSNBCDE	NBCG	~	CIS	SCH35	F11		F04
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		Score	154	977.	72.	97	70.		93	04.	•	n o		98.	31.	81.	0 d	9 -	່ດ	8	•	ω΄		י ת	o u		ū.		σ,				٠ ج	8	.i.			6	89.2	00
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ALIGNMENTS

Streptomyces sp. SK strain xylA gene. Y15518 Tissel. GI:4210848 XylA gene.

01-FEB-1999

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GTTCCGTCAGGCGCTCGACGCGACCGCATGACCGTTCCGATGGCCACCACCAACCTCTT
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   cgacqacqacctgatccccttcqgqqcgtccqacacccgagcgcgaggcgcacqtcaagcg
                                421 CGACGACGACCTGATCCCCTTCGGGGCGTCCGACACCGAGCGCGAGGCGCACGTCAAGCG
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Streptomyces sp.
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.

[ (bases 1 to 1546) Belghith-Srih, K.
Unpublished 2 (bases 1 to 1546) Belghith-Srih, K.
Direct Submission
Submitted (24-NOV-1997) K. Belghith-Srih, Centre de Biotechnologie
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/FC_funtion="conversion of D-xylose 10.5%
D-glucose to D-fructose"
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263. .1423
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AFDLLGEVYTSQGYDLRFALERFRENGREGAESTRARDFRWE
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SACYEGPRHFDFKPPRTEDLGVWAAAAAGCMRNYLIKERAAAFRADPFVQAALRASR
LDQLAQPTAADGLEDLLADRAAFEDFDVEAAAARGMAFERLDQLAMDHLLGARG"
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Joo.G.J., Shin, J.H., Heo.G.Y., Park, H.D. and Rhee, I.K.
Direct Submission
Submitted (19-JUL-1999) Department of Agricultural Chemistry,
College of Agriculture, Kyungpook National University,
Sankyuk-Dong, 1372, Taegu 702-701, Korea
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Streptomyces chibaensis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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Pred. No. 1.6e-84;
0; Mismatches 176; Indels
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D-xylose isomerase (xylA)
         1546
1. .1952
/organism="Streptomyces chibaensis"
/strain="J-59"
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Streptomyces rubiginosus DNA.
Streptomyces rubiginosus DNA.
Streptomyces rubiginosus DNA.
Streptomyces rubiginosus
Bacteria: Firmicutes: Actinobacteria: Actinobacteridae;
Actinomycetales: Streptomycineae; Streptomycetaceae; Streptomyces.
1 (bases 1 to 3060)
Wong, H.C., Ting, Y., Lin, H.-C., Reichert, F., Myambo, K., Watt, K.,
Toy, P. L. and Drummond, B.,
Genetic organization and regulation of the xylose degradation genes
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AGRESPPROMEDALCEALRQCGEAAHEAANSIGGQQHGUTYLLDGHGEPVRRALLMND
VRSAPQGHRLI EELGGAKFWAERTGSVPAASFTVKWAMLAEHEPEAVRATRAVRLPH
DYLTERLGGGGTTDRODASGTGWASGTEATDEELICHYGLDPALLPRVVRPGEVAGT
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GTVAGFADARGDHLPLGYTLVTLATLAALDLGDREAVERGHGYTLLPFLGGERTP
NLPRSSGLIHGLRHPTGGQLLQAAVGGAYSGLAALDLVLDEBADPSAPLLIGGGRTP
NLPRSSGLIHGLRHPTGGQLLQAAVGGAYSGLAALDLYLDEBADPSAPLLIGGGRTP
RGTAMQQTVRRLSGRAVQVPRAAELVALGAAQAAGLLTGGBDAAVARRWETAAGPVL
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Streptomyces rubiginosus xylose kinase and xylose isomerase genes,
complete cds.
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/db_xref="taxon:1929"
complement(88. .1659)
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/gene="xylA"
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J. Bacteriol. 173, 6849-6858 (1991)
92041569
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complement(139. .1584)
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complement(88. .126)
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                                                                                                                         63.2%; Score 977.2; DB 1;
1larity 87.4%; Pred. No. 8.9e-80;
Conservative 0; Mismatches 153;
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                                                                                                                                             Matches 1106;
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Strotlaceoniger DNA.

Streptomyces isolaceoniger
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.

1 (bases 1 to 1201)

Drocourt, D., Bejar, S., Calmels, T., Rey, J. and Tiraby, G.

Nucleotide sequence of the xylose isomerase gene from Streptomyces
                                                                          1254
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                                                                                                                                                                                                                                 gene,
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S.violaceoniger xylose isomerase
M36269
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/db_xref="taxon:1953"
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DEFINITION ACCESSION VERSION KEYWORDS SOURCE

RESULT STMXYLI LOCUS

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AUTHORS TITLE

JOURNAL MEDLINE

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FEATURES

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//bb_xref="GI:48005"
//bb_xref="SWISS-PROT" P09033"
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GFTANDRDAFRARTIRNIDIAABELGAKTYVAMGGREGASGGGAKTVDRALDRWKE
AFDLIGEYVTANGY DULFFAIRNIDIAABELGAKTYVAMGGREGASGGAKTVDRALDRWKE
GHEQMAGLNFPHGIAQALWAGKLFHIDLNGGSGIKYDQDLRFGAGDLRAAFFUNDLLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAGYEGPRHFDFKPPRTEDFDGVWASAEGCMRNYLILKERAARFRADFEVQEALRAAR
LDQLAQPTAADGLEALLADRTAFEDFDVEAAARRAWPFERLDQLAMDHLLGARG"
454 c 403 g 158 t
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                                                                                                                                                                                                                                                                                                                        Drocourt, D., Bejar, S., Calmels, T., Reynes, J.P. and Tiraby, G. Nucleotide sequence of the xylose isomerase gene from Streptomyces
                                                                                                                                                                                                                                      Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces (bases 1 to 1202)
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                                                                                                                         SVXYL 1202 bp DNA BCT 18-JUL-1995 Streptomyces violaceoniger xylA gene for D-xylose-isomerase tetramer alpha 4 ; EC 5.3.1.5).
X12816 X12816.1 GI:48004
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Pred. No. 4.7e-79;
0; Mismatches 110; Indels
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                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
1. .1202
Actainsm="Streptomyces violaceoniger"
strain="CBS 409-73"
/db_xref="taxon:1953"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="pot. ribosome binding site"
25. .1194
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ccgcgtacgaggacttcgacgtggacgcggc
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Submitted (09-SEP-1988) Drocc
31094 Toulouse Cedex, France
2 (bases 1 to 1202)
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Streptomyces violaceoniger.
Streptomyces violaceoniger
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/note="Method: conceptual translation with partial peptide sequencing. This sequence comes from Fig. 2; X1"
/codon_start=1
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/db_xref="G1:786340"
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ELGAHGVTFHDDDLIPFGATDSERAEHIKRFRQGLDETGMKVPMATTNLFTHPVFKDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GFTANDRDVRRYAVRKTIRNIDLAVELGAQTYVAWGGREGAESGAAKDVRVALDRMKE
AFDLLGEYVTSQGYDTPFAIEPKPNEPRGDILLPTIGHALAFIDGLERPELYGVNPEV
GHEQWAGLINFHGIAQALMAGKLFHIDLNGQSGYTYDQDLRFGPGDLAAAFWIVDLLE
SAGYEGPRHFPFRPFREDFDGVWAAGGKMYLILKERAAFRADPEVQEALRAAR
LDELAQPTAGGLGLLPBRSFEDFDPAAARGMAFELLDGLAMDHLLGARG

566 c 2 others
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Wang, Y., Huang, Z., Dai, X., Liu, J., Cui, T., Niu, L., Wang, C. and Xu, X.
    Genomic
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Location/Qualifiers
1. 1522
/organism="streptomyces diastaticus" /db_xref="taxon:1956" |
193. .1359
/general space of the complete of the compl
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                                                                                                             Streptomyces diastaticus No. 7 M1033.
Streptomyces diastaticus
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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Pred. No. 4.4e-79;
0; Mismatches 204; Indels 9;
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  diastaticus,
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  [Streptomyces
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Best Local Similarity 84.3%;
Matches 1141; Conservative (
xylose isomerase [Str
1522 nt].
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873809.1 GI:786339
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomyces. 5 Actinomycetales; Streptomycineae; Streptomyces. 1 (bases 1 to 1164)
Akaza,M., Kitazawa,M., Oki,K. and Nakao,Y.
Akaza,M., Kitazawa,M., Oki,K. and Nakao,Y.
PERPARATION OF GLUCOSE ISOMERASE INCREASED IN HEAT RESISTANCE Patent: JP 199084956-A 07-APR-1998;
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PI AKAZA MASAHIRO, KITAZAWA MASARU, OKI KENICHI, NAKAO YOSHIMI 1 C12N9/92,C07H21/04,C12N15/09,(C12N9/92,C12R1:19),(C12N15/09, PC C12R1:465);
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GHEQWAGLNFPHGIAQALWAGKLFHIDLNGGSGIKYDOOLRFGAGDRAFRLVDLLE
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                                                         Bacteria: Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomyces. Actinomycetales; Streptomycineae; Streptomyces. I (bases 1 to 1164)
Luiten,R.G.M., Quax,W.J., Schuurhuizen,P.W. and Mrabet,N.
Novel glucose isomeraes enzymes and their use
Patent: EP 0351029-A 16 17-JAN-1990;
GIST-BROCADES N.V.; PLANT GENETIC SYSTEMS, N.V
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Pred. No. 2e-77;
0; Mismatches 112;
                                                                                                                                                                                          /organism="Streptomyces murinus"
/db_xref="taxon:33900"
                                                                                                                                                           Location/Qualifiers
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glucose isomerase.
Streptomyces murinus.
Streptomyces murinus
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89.9%;
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Drummond,R.J., Bloch,W., Matthews,B.W., Toy,P.L. and Nicholson,H.H.
PROCARYOTIC XYLOSE ISOMERASE MUTEINS AND METHOD TO INCREASE PROTEIN
                                                                                                                           02-DEC-1994
                                                                                 440 ttcgggggggtccgacaccgagcgcgaggcgcacgtcaagcggttccgtcaggcgctcgac
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                                                                  CCCCCCGACCCGGAGGTGCAGGAGGCCCTGCGCCCCGCGCGTCTGGACCAGCTGGCCCCAG
                                                                                                                   gacgtggacgcg---gccgcgcgcggcatggccttcgagcgcctcgaccagctcgccatg
GAGGGCCCGCGCGCACTTCGACTTCAAGCCGCCGCGGACCGAGGACTTCGACGCCGTGTGG
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Pred. No. 7.6e-76;
0; Mismatches 125; Indels
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Location/Qualifiers
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426 c 405 g
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Best Local Similarity 88.8%;
Matches 1036; Conservative
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                                                                                                                                                                                                                                                                 Unknown.
Unclassified.
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DEFINITION
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SOURCE
ORGANISM
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ORIGIN
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VERSION
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TITLE
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6
                                                                                           Length 1164;
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   /product='glucose isomerase'
Location/Qualifiers
1. .1164
Streptomyces
                                                                                         1.3%; Score 947.8; DB 5; Similarity 90.1%; Pred. No. 5.5e-77; 11; Conservative 0; Mismatches 107;
                                        /organism="Streptomyces rochei"
/db_xref="taxon:1928"
441 c 387 g 155 t
 /organism=′
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Matches 1051;
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                                                          COUNT
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C12N15/00,C12N1/16,C12N1/20,C12N9/92,(C12N9/92,C12R1:19),
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Pred. No. 3.1e-73;
0; Mismatches 264; Indels
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666. .1850
/product-'glucose isomerase'
R 1851. .>2010.
Location/Qualifiers
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/organism="Streptomyces rochel"
/db_xref="taxon:1928"
1 757 c 673 g 288 t
                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                     C12R1:125), (C12N9/92, C12R1:865);
                      Streptomyces griseofuscus
JP 1989137979-A/1
30-MAY-1989
24-NOV-1987 JP 1987295739
                                                                                                                                                                                                                                                                                                          *source: strain=S-41;
                                                                                                                                                                                                             strandedness: Double;
                                                                                                                                                                                                                                   topology: Linear;
hypothetical: No;
anti-sense: No;
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Best Local Similarity 81.0%;
Matches 1226; Conservative (
NATL FOOD 10S STEEP 10D 30-MAX 30-MAX
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Actinomycetales; Streptomycineae; Streptomyces.

(bases 1 to 2010)

Fukazawa,C. and Kainuma,K.

GLUCOSE ISOMERASE GENE, RECOMBINANT HAVING SAID GENE AND

MICROORGANISM CONTAINING SAID RECOMBINANT

Patent: JP 1989137979-A 1 30-MAY-1989;
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                                              361 CGCAACATCGACCTCGCGGTCGAGCTCGGCGCCGAGACCTATGTGGCCTGGGGCGGCCGC
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                                             l (bases I to 1892)
Saari,G.C., Kumar,A.A., Kawasaki,G.H., Insley,M.Y. and O'Hara,P. Sequence of the Ampullariella sp. strain 3876 gene coding for xylose isomerase
J. Bacteriol. 169 (2), 612-618 (1987)
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Micromonosporineae; Micromonosporaceae, Actinoplanes.

1 (bases 1 to 1892)
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                                                                                                                                                                                                                                                       /organism="Actinoplanes ATCC31351
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/note="putative"
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Pred. No. 5e-46;
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1 (bases 1 to 1639)
Amore,R. and Hollenberg,C.P.
Direct Submission
Submitted (07-AUG-1989) Amore R., Hollenberg C.P., Institut f
Mikrobiologie, Universitaetsstr 1 Geb. 26.12, 4000 Duesseldorf
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Amore,R. and Hollenberg,C.P.
Xylose isomerase from Actinoplanes missouriensis: job the gene and the protein
Nucleic Acids Res. 17 (18), 7515 (1989)
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/note="put. prokaryotic promoter element"
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Aorganism="Actinoplanes missouriensis"
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Ab_xref="taxon:1866"
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Aclone="PRA1"
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Direct Submission
Submitted (16-OCT-1989) to the
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NGPDGAPAYDGPRHFDYKPSRTEDYDGVWESKKANIRMYLLIKERAKARADPEVOEA
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               CATCGACCTGAACGGTCAGCACGGCCCGAAGTTCGACCAGGACCTGGTCTTCGGCCACGG
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    /organism="synthetic construct"
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/protein_id="caA0053.1"
/db_xref="GI:4526609"
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ECOAMÍ (DSM) GI
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Score 598.8; DB 5;
Pred. No. 6.6e-46;
0; Mismatches 302;
     38.7%;
72.0%;
                                                        Best_Local Similarity 72.0
Matches 847; Conservative
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BIGAYGTTFPDDLVPFSGSAQTRGDIAGFKALDEFGLIPWTTHTHPVFKDG
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BITSKURSVRRKALRYUKGMDLGAELGAFTLVLWGRREGAEYDSAKDVSALDFRTE
ALNLLAQYSEDRGYGLRFAIEPKPNEPRGDILLPTAGHAIAFVQELERPELFGINPET
BIGANSVRPTGAGALMYKLFFIDDNGQHGFFRQQDLYFGHGDLLARFSLVDLLB
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LAASKVAELKTPTLNOGGGYAELLADRSAFEDYDADAVGAKGFGFVKLNOLAIEHLLG
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                                          -ggccgcgcgcgcatggccttcgagcgcctcga
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Actinoplanes missouriensis.
Actinoplanes missouriensis
Bacteria; Firmicutes; Actinobacteria, Actinobacteridae;
Actinomycetales; Micromonosporineae; Micromonosporaceae;
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Luiten, R.G. M., Quax, W.J., Schuurhuizen, P.W. and Novel glucose isomerase enzymes and their use Patent: EP 0351029-A 14 17-7AN-1990;
GIST-BROCADES N.V.; PLANT GENETIC SYSTEMS, N.V
                                                                                                                                                                                                                                                                                                                                           missouriensis"
                                                                                                                                                           DNA PAT glucose isomerase.
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Pred. No. 7.2e-46;
0; Mismatches 301;
                                                                                /organism-"Actinoplanes missou
/db_xref-"taxon:1866"
/ ->1182
/codon_state1
/transl_table=11
/product-"glucose isomerase"
/protein_id="CAAO0884.1"
/db_xref-"SWISS_PROT:P12851"
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A.missouriensis DNA for
A10241
A10241.1 GI:490200
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Local Similarity 72.1%;
es 846; Conservative
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gttcaccgccaacgaccgcgcagtgcgccgttacgccctgcgcaagaccatccggaacat
                                                                                       309 cricaccagcaacgaccerrccrecececracecearccecaagerecrececagar
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Search completed: March 22, 2000, 23:29:30 Job time: 1477 sec

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Complete sequence Glucose isomerase Amino acid sequenc Glucose isomerase Glucose isomerase
                                                                                                                                                 March 22, 2000, 23:30:34 ; Search time 27.38 Seconds
(without alignments)
333.924 Million cell updates/sec
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Xylose Isomerase g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                            US-09-383-318-2
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1 MNYQPTPEDRFTFGLWTVGW......GMAFERLDQLAMDHLLGARG 386
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
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eryA region polype A. mediteranei ri Amino acid sequenc Amino acid sequenc M. leprae 65 kDa p Sequence encoded b Shaker-11ke potass HSV-2 strain SB5 C M. tuberculosis 65 Microbispora therm HSV-2 strain SB5 C	ALIGNMENTS R02215 standard; protein; 388 AA. R02215 standard; protein; 388 AA. R02215. 23-AUG-1990 (first entry) Sequence encoding Streptomyces murinus DSM 40091 (Smu) glucose isomerase; Streptomyces murinus DSM 40091. Streptomyces murinus. Streptomyces murinus. 17-JAN-1990. 17-JAN-1990. 17-JAN-1990. 17-JAN-1990. 17-JAN-1990. 18-YOL-1989; 201892. 17-JAN-1990. 18-YOL-1989; 201892. 20	tch al Similarity 93.6%; Score 1900; DB 1; Length 388; al Similarity 92.8%; Pred. No. 3.46-171; 360; Conservative 14; Mismatches 12; Indels 2; Gaps 360; Conservative 14; Mismatches 12; Indels 2; Gaps MNYOPTEDRITEGLWTWGWOGEDPFCDATRPALDPVD-VORLAELGANGVTFHDDDLIP 59 1::
R444430 R548450 R04715 R04716 R23383 W72333 R64766 W72033	ALIGNME 88 AA. ces murinus yces murinu yces murinu an-). huizen PW, I huizen PW, I anti quicos cantinu tant quicos	Score Pred. 14; Mis. RDFEGDAT
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3398 4572 572 572 572 800 329 921 973 1896	st entry) Streptomyces m Streptomyces m Streptomyces m Streptomyces m Streptomyces m Streptomyces Streptomyce	93.6% y 92.8%
NN N 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	ndard; p 0 (firs 00 (fir	nilarity Conserv Conserv IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
0 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	RESULT 1 AC R02215 ID R02215 C R02215 DI 23-AUG-1990 (first entry be sequence encoding Strepton be isomerase (GI) KW Glucose isomerase; Strepton by Strepton by Strepton by Di-JAN-1990 Di-JAN-1990 PP II-JUL-1989; 201892. PR (KONN) Gist-Brocades NV PI (MISON-1988; EP-402789. PR (KONN) Gist-Brocades NV PI (MISON-1988). PR (KONN) Gist-Bro	
WWWWWW44444 BWDLWWWOLUW45	COCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	Match Match Match
	X X L Y L L L L L X X Y Y Y Y Y Y Y Y Y	2

Xylose isomerase g BglII fragment con Xylose isomerase g Barley xylose isom

Xylose isomerase x

Glucose isomerase Sequence encoding Xylose isomerase g

Thermus aquaticus Glucose isomerase Hyperthermostable

R03030 R22623 R44236 W26508 R22720 R03024

862 320 275.5 275 275 272.5 255.5

Glucose isomerase

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New mutant glucose isomerase enzymes -
obtd. by site-directed mutagensis of gene from Actinoplanes
missouriensis, used for produ. of high fructose corn syrups
missouriensis, spp; English.
The invention is a novel mutant glucose isomerase (GI) enzyme with
improved properties thru AA substitu. The GI is pref. derived from
Actinoplanes missouriensis. The substitu. is Lys for Arg.
sources.
                                                                              Glucose isomerase; Streptomyces violaceoniger CBS 409.73 Streptomyces violaceoniger.
                                                Sequence encoding Streptomyces violaceoniger CBS 409.73
                                                                                                                        17-JAN-1990.
17-JUL-1989; 201892.
04-NOV-1988; EP-402789.
Luiten RGM, Quax WJ, Schuurhuizen PW, Mrabet
WPI; 90-016368/03.
    standard; protein; 389 AA.
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Matches 354; Conservative
                                 23-AUG-1990 (first entry)
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                                                                                                                                                                                                                                                                                                                                                              389 AA;
                                                                 isomerase (GI)
                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Improving heat resistance of glucose isomerase - comprises replacing part of amino acid in specific position of amino acid sequence Claim 1; Fig 1; 7pp; Japanese This represents a Streptonyces glucose isomerase that can be used to create a mutant with improved heat resistance which comprises replacing an amino acid in a specific position of the sequence. The Sequence 387 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MNYQPTPEDRFTFGLWTVGWQGRDFFGDATRPALDPVD-VQRLAELGAYGVTFHDDDLIP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LFHIDLNGQSGIKYDQDLRFGAGDLRAAFWLVDLLESAGWEGPRHFDFKPPRTEDIDGVW
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                                                                                                                                  21-SEP-1998 (first entry)
S. griseofuscus glucose isomerase.
S. driseofuscus glucose isomerase.
Stromerised sugars.
Streptomyces griseofuscus.
                                                                                                                                                                                                                 ocation/Qualifiers
1. 387
note= "mature protein"
                                                                                                                                                                                                                                                                                 'note= "encoded by GAC"
                                                                                                                                                                                                                                                                                                380
/note= "encoded by GAC"
DVD-AAARGMAFERLDQLAMDHLLGARG 386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 91.8
Matches 356; Conservative
                                                                                                                                                                                                                                                                                                                                                        12-SEP-1996; 262370.
12-SEP-1996; JP-262370.
(GODO) GODO SHUSEI KK.
WPI: 98-264846/24.
N-PSDB: V32494.
                                                                                                                                                                                                                                                                 Misc_difference 143
                                                                                                                                                                                                                                                                                                Misc_difference
                                                                                                                                                                                                                                    Protein
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60 FGASDTEREAHVKRFRQALDATGMTVPMATTNLFTHPVFKAGAFTANDRAVRRYALRKTI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 RNIDLAVELGAKVYVAWGGREGAESGAAKDVRAALDRMKEAFDLLGEYVTSQGYDIRFAI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EPKPNEPRGDILLPTIGHALAFIERLERPELYGVNPEVGHEQMAGLNFPHGIAQALWAGK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LFHIDLNGQSGIKYDQDLRFGAGDLRAAFWLVDLLESAGWEGPRHFDFKPPRTEDIDGVW 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Nav deduced sequence of Streptomyces rubiginosus xylose isomerase
Streptomyces rubiginosus xylose isomerase; mutein; fructose;
xylulose; sweeteners.
                                                                                                                          .
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92.0%; Score 1867.5; DB 1; Length 389; 91.0%; Pred. No. 4e-168; ive 16; Mismatches 16; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DVDAAARGMA - - FERLDQLAMDHLLGARG
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10-AGG-1988; UO2765.
22-MAR-1988; US-17163; US-084479.
(CETU) Cetus Corp (UYOR-).
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LID DT 110
DDT 110
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12-SEP-1996; 262370.
12-SEP-1996; JP-262370.
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created by
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These muteins are used to convert glucose to fructose, and xylose to xylulose, ed n mfr. of sweetners. Compared with native xylose the muteins have different chemical and thermal stability, kinetic constants, specificity and/or lower optimum pH. Amino acid substitution sites are selected by first determining, from the crystallographic structure, the phi and psi angles, then screening these for values within the specified ranges eg a site which has a phi backbone configuration angle -40 to 95 degrees when psi - 120 to 180 degrees, and is able to accommodate A without distortion of the 3-D protein structure, so that the substitution decreases the configurational entropy of unfolding CEU; or replacing the CEU.

Sequence 388 AA:
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                             Increasing stability of proteins by specific aminoacid replacement where aminoacid introduced decreases configuration entropy of
                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "mature wild-type Tyr is replaced with Phe"
                                                                                                                                                                                                                                                                                              MNYQPTPEDRFTFGLWTVGWQGRDPFGDATRPALDPVD-VQRLAELGAYGVTFHDDDLIP
                                                                                                                                                                                                                                                                                                           LFHIDLNGQSGIKYDQDLRFGAGDLRAAFWLVDLLESAGWEGPRHFDFKPPRTEDIDGVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 ASAAGCMRNYLILKERAAAFRADPEVQEALRASRLDELARPTAADGLHPLLDDRSAFEEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ASAAGCMRNYLILKERAAAFRADPEVQEALRAARLDQLAEPTAADGLQALLADRTAYEDF
                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                      Length 388;

    S. griseofuscus glucose isomerase mutant Y252F.
    Glucose isomerase; heat resistance; thermostable; mutant;

                                                                                                                                                                                                                                                                          Indels
Matthews BW, Toy PL, Nicholson
                                                                                                                                                                                                                                                    92.0%; Score 1867; DB 1;
91.8%; Pred. No. 4.4e-168;
iive 14; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DVD-AAARGMAFERLDQLAMDHLLGARG 386
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                                                            134pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W63618 standard; Protein; 387
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                                                                                                                                                                                                                                                    Query Match 92.0
Best Local Similarity 91.8
Matches 356; Conservative
Bloch W,
                                                 unfolding of protein
Drummond RJ, Bloch WPI; 89-068875/09.
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                     PSDB; N91083
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21-SEP-1998
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                                                           Disclosure;
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                                                 Improving heat resistance of glucose isomerase - comprises replacing part of amino acid in specific position of amino acid sequence [Claim 1; Page : , 7pp; Japanese.
This represents a mutant of Streptomyces glucose isomerase that has improved heat resistance. The mutant was created by replacing an amino acid in a specific position of the mature wild-type sequence. The glucose isomerase is useful for the preparation of isomerised
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MNYQPTPEDRFTFGLWTVGWQGRDFFGDATRPALDPVD-VQRLAELGAYGVTFHDDDLIP
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obtd. by site-directed mutagensis of gene from Actinoplanes
missouriensis, used for prodn. of high fructose corn syrups
Disclosure, 56pp; English.
The invention is a novel mutant glucose isomerase (GI) enzyme
improved properties thru AA substitu. The GI is pref. derived
Actinoplanes missouriensis. The substitu. is Lys for Arg.
                                                                                                                                                                                                                                                                                                                                                                                               Length 387;
                                                                                                                                                                                                                                                     sequence is not provided in the specification; it modifying the glucose isomerase sequence provided 387 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glucose isomerase; Streptomyces violaceoruber LMG 7183
                                                                                                                                                                                                                                                                                                                                                                                               91.8%; Score 1863.5; DB 1; 91.5%; Pred. No. 9.4e-168; ive 17; Mismatches 13; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ż
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EP-351029-A.
17-JAN-1990.
17-JUL-1988.
EP-402789.
(KONN) Gist-Brocades NV (Plan-).
Luiten RGM, Quax WJ, Schuurhuizen FW, Mrabet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  360 DVD-AAARGMAFERLDQLAMDHLLGARG 386
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(GODO ) GODO SHUSEI KK.
WPI; 98-264846/24.
                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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240 LFHIDLNGQSGIKYDQDLRFGAGDLRAAFWLVDLLESAGWEGPRHFDFKPPRTEDIDGVW 299
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11-JAN-1990.

10-JAN-1990.

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                                                                                                                                                                          1 MNYQPTPEDRFTFGLWTVGWQGRDPFGDATRPALDPVD-VQRLAELGAYGVTFHDDDLIP 59
 GI from different
                                                                                                                                                                                                                                              EPKPNEPRGDILLPTIGHALAFIERLERPELYGVNPEVGHEQMAGLNFPHGIAQALWAGK
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                                                                                                                                                        1 MNYQPTPEDRFTFGLWTVGWQGRDFFGDATRPALDPVD-VQRLAELGAYGVTFHDDDLIP
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                                                                                  Length 387;
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                                                                                                                      17; Indels
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Yjlose isomerase gene of Streptomyces violaceoniger.

Ylose isomerase; Arthobacter.
Streptomyces violaceoniger.

MO9000196-A.
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 compares AA sequences of
                                                                                  Query Match 91.6%; Score 1859; DB 1; Best Local Similarity 91.2%; Pred. No. 2.5e-167; Matches 353; Conservative 15; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86.0%; Score 1744.5; DB 1.
larity 87.2%; Pred. No. 1.5e-156;
Conservative 18; Mismatches 9;
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or vice versa. Figure 21 sources.
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Best Local S
Matches 340)
                                  Sequence
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T1-JUL-1989; 201892.

R 04-NOV-1988; EP-402789.

(KONN) Gist-incondes NV (Plan-).

Luiten RGM, Quax WJ, Schuurhuizen PW, Mrabet N;

Luiten RGM, Quax WJ, Schuurhuizen PW, Mrabet N;

WPI; 90-016368/03.

The wm untant glucose isomerase enzymes - obtd. by site-directed mutagensis of gene from Actinoplanes obtd. by site-directed mutagensis of gene from Actinoplanes of an isocuries; 56pp; English.

C The invention is a novel mutant glucose isomerase (GI) enzyme with improved properties thru AR substitn. The GI is pref. derived from Actinoplanes missocuriensis. The substitn. is Lys for Arg.

C Or vice versa. Figure 21 compares AA sequences of GI from different
                                                                                                                                                                                                                              LPHIDLNGQSGIKYDQDLRFGAGDLRAAFWLVDLLESAGWEGPRHFDFKPPRTEDIDGVW 299
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence encoding Streptomyces thermovulgaris DSM 40444 (Sth) glucose isomerase (GI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RNIDLAVELGAKVIVAWGGREGAESGARDVRAALDRAKEAFDLLGEIVTSQGYDIRFAI 179
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                                                                                                                                                                                                                                                                                                                                                 RNIDLAVELGARTYVAWGGREGAESGAAKDVRAALDRMKEAFDLLGEYVTSQGYDIRFAI 180
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RNIDLAVELGAKVYVAWGGREGAESGAAKDVRAALDRMKEAFDLLGEYVTSQGYDIRFAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MNYQPTPEDRFTFGLWTVGWQGRDFFGDATRPALDPV-DVQRLAELGAYGVTFHDDDLIP
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84.5%; Score 1715.5; DB 1; Length 345;
Best Local Similarity 93.6%; Pred. No. 7.1e-154;
Matches 323; Conservative 14; Mismatches 7; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glucose isomerase; Streptomyces thermovulgaris DSM 40444
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EPKPNEPRGDILLPTIGHALAFIERLERPELYGVNPEVGHEQMAGLNFPHGIAQALWAGK 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RNIDLAVELGAKVYVAWGGREGAESGAAKDVRAALDRMKEAFDLLGEYVTSQGYDIRFAI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xylose isomerase mutants - having amino acid replacements to improve activity under acid pH conditions and/or increase stability and/or affinity for metal ions. Disclosure; Fig 7; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MNYQPTPEDRFTFGLWTVGWQGRDPFGDATRPALDPVD-VQRLAELGAYGVTFHDDDLIP 59
                                                                                                                                                     New mutant glucose isomerase enzymes -
obtd. by site-directed mutagensis of gene from Actinoplanes
missouriensis, used for prodn. of high fructose corn syrups
Disclosure; ; 50pp; English.
The invention is a novel mutant glucose isomerase (GI) enzyme with
improved properties thru AA substitn. The GI is pref. derived from
Actinoplanes missouriensis. The substitn. is Lys for Arg.
or vice versa. Figure 21 compares AA sequences of GI from different
                                                                                                                                                                                                                                                                                                                                                                                                                                                            LFHIDLNGQSGIKYDQDLRFGAGDLRAAFWLVDLLESA-----GWEGPRHFDFKPPRTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IDGVWASAAGCMRNYLILKERAAAFRADPEVQEALRAARLDQLAEPTAADG--LQALLAD
                                                                                                                                                                                                                                                                                                                                                                   Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                        78; Indels
Ampullariella species ATCC 31351.
                                                                                                                                                                                                                                                                                                                                                                   67.1%; Score 1361.5; DB 1
66.5%; Pred. No. 1.9e-120;
ive 45; Mismatches 78;
                                                   17-JAN-1990.
17-JUL-1989; 201892.
04-NOV-1988; P4-402789.
CA-NOV Gist-Brocades NV (Plan-).
Luiten RGM, Quax WJ, Schuurhuizen PW, Mrabet
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04-JUL-1989; G00748.
04-JUL-1988; GB-015902.
(BLOW) Blow D M.
Blow DM, Hartley BS, Henrick K.
WPI; 90-037131/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R03029 standard; protein; 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xylose isomerase gene of Ampu
Xylose isomerase; Arthobacter
Ampullariella sp. strain 3876
WO9000196-A.
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                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 66.5
Matches 262; Conservative
   isomerase;
                                                                                                                                                                                                                                                                                                                  394 AA;
                                                                                                                                        WPI; 90-016368/03
                  Ampullariella.
EP-351029-A.
                                                                                                                                                                                                                                                                                                                    Sequence
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R03029
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61 FGSSDTERESHIKRFRQALDATGMTVRMATTNLFTHPVFK-DRFTANDRDVRAYAVRKTI 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LFHIDLNGQSGIKYDQDL---RFGAGDLRAAFWLVDLLESAGWEGPRHFDFKPPRTEDID 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240 LFHIDLNGQSGIKYDQDCGSRRRPAGGV----LVVDLLESAGYEGPRHFDFKPPRTEDFD 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GVWASAAGCMRNYLILKE-------RAAAFRADPEVQEALRAARLDQLAEPTAA 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GVWASAEGCMRNYLILKQPRPPSAPTRRCRRRASA----PRVWTSWPSRPL-----A 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MNYQPTPEDRFTFGLWTVGWQGRDPFGDATRPALDPVD-VQRLAELGAYGVTFHDDDLIP
                                                                                                                                                                                                                                                                                                                                                                                                  Novel glucose isomerase gene
- exists in chromosome of Streptomyces and is contained in recombinant etc.
Claim i, fig 1, 6pp; Japanese.
Glucose isomerase from Streptomyces spp. (see N90362). Used to study this protein's structure by recombinant techniques, and for sequence 394 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EPKPNEPRGDILLPTIGHALAFIERLERPELYGVNPEVGHEQMAGLNFPHGIAQALWAGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-AUG-1990 (first entry)
Sequence encoding Ampullariella species ATCC 31351 glucose
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                                                                     301 ASAAGCMRNYLILKERSAAFRADPEVQEALRASRLDQLAQPTAAD 345
                                                 300 ASAAGCMRNYLILKERAAAFRADPEVQEALRAARLDQLAEPTAAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 75.4%; Score 1530.5; DB 1; Best Local Similarity 79.0%; Pred. No. 2.3e-136; Matches 305; Conservative 21; Mismatches 25;
                                                                                                                                                                                                      1-NOV-1989 (first entry)
Streptomyces spp. glucose isomerase
Glucose isomerase; Streptomyces; DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DGLQALLADRTAYEDFDVD-AAARGM 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R02213 standard; protein; 394 AA.
                                                                                                                                                                       P90423 standard; protein;
                                                                                                                                                                                                                                                                                                              24-NOV-1987; 295739.
24-NOV-1987; JP-295739.
(NORQ) Norinsho.
                                                                                                                                                                                                                                                                                                                                                                   WPI; 89-198224/27.
N-PSDB; N90362.
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                                                                                                                                                                                                                                                               Streptomyces
J01137979-A.
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complete sequence of wildtype (WT) Actinoplanes missouriensis
glucose isomerase (GT)
Site-directed mutagenesis; glucose isomerase; Actinoplanes missouriensis;
Migh fructose corn syrup.
Actinoplanes missouriensis.
EP-331029-A.
Mutants of the xylose isomerase (XI) gene esp. Arthobacter strain B3728, have been shown to have increased thermal stability, and/or improved activity at low pH, and/or affinity for metal ions esp. Ca. Useful in industrial conversion of glucose to sweeter sugars.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 FGADAATRDGIVAGFSKALDETGLIVPMYTTNLFTHPVFKDGGFTSNDRSVRRYAIRKVL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EPKPNEPRGDILLPTIGHALAFIERLERPELYGVNPEVGHEQMAGLNFPHGIAQALWAGK 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 RNIDLAVELGAKVYVAWGGREGAESGAAKDVRAALDRMKEAFDLLGEYVTSQGYDIRFAI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LFHIDLNGQSGIKYDQDLRFGAGDLRAAFWLVDLLESA-----GWEGPRHFDFKPPRTED 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  295 IDGVWASAAGCMRNYLILKERAAFRADPEVQEALRAARLDQLAEPTAADG--LQALLAD 352
                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                       MNYQPTPEDRFTFGLWTVGWQGRDPFGDATRPALDPVD-VQRLAELGAYGVTFHDDDLIP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LFHIDLINGOHGPKFDQDLVFGHGDLLNAFSLVDLLENGPDGGPAYDGPRHFDYKPSRTED
                                                                                                                                                                                                                                      6
                                                                                                                                                                                    Length 394;
                                                                                                                                                                                 66.7%; Score 1353.5; DB 1; Length
66.0%; Pred. No. 1.1e-119;
.ive 46; Mismatches 79; Indels
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                                                                                                                                                                                    Query Match
Best Local Similarity 66.0°
Matches 260; Conservative
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                                              Gaps
                                                                                                                          9
                                                                                  1 MNYQPTPEDRFTFGLWTVGWQGRDPFGDATRPALDPVD-VQRLAELGAYGVTFHDDDLIP 59
                                                                                                         EPKPNEPRGDILLPTIGHALAFIERLERPELYGVNPEVGHEQMAGLNFPHGIAQALWAGK
                                                                                                                                                                                                                                                                                                                                                                                                             LFHIDLNGQSGIKYDQDLRFGAGDLRAAFWLVDLLESA-----GWEGPRHFDFKPPRTED
                                            6
    Length 394;
                                            Indels
    DB 1;
                                            16;
    Score 1351.5; DB 1
Pred. No. 1.7e-119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glucose isomerase mutant 425K.
GI; high fructose corn syrup; sweetener; sugar.
Actinoplanes missouriensis.
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49. .52
/label= beta_strand
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/label- beta_strand
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/label= helix
127. .239
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.276
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66.6%;
65.5%;
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/label= hr
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'label- he
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/label- be
                                            Conservative
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264. 276
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/label= }
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Matches 258; Conserv
    Query Match
Best Local
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                                                                                         Or JAN-1991; EP-200029.

ROJAN-1991; EP-200003.

ROJAN-1991; EP-200003.

ROL-JAN-1991; EP-200003.

ROLAN-1991; EP-200003.

ROLAN-1991; EP-200003.

ROLAN-1991; EP-200003.

Lambeir AVR. Quax WJ. Lasters Iv. Van der Laan JM;
Lambeir AVR. Quax WJ. Lasters Iv. Van der Laan JM;
Lambeir AVR. Quax WJ. Lasters Iv. Van der Laan JM;
ROLAN-19193/32.

ROLCOSE isomerase mutants with altered substrate specificity -
and methods for selecting aminoacid(s) for substrate specificity -
and methods for selecting aminoacid(s) for substrate specificity -
and methods for selecting aminoacid(s) for substrate specificity -
ciaim 13; Page 13; 18pp; English.

The analogue was preped by site directed mutagenesis of the GI
gene. The substrance of fo-8A of the 01, 02 and 03 positions of the
substate in the enzyme-sorbitol-cobalt complex. This causes
disruption of the water structure in the interface and displaces
construction of the water structure in the interface and displaces
construction by the substrate. This gives the enzyme a
calibhatic hydrogens of the substrate. This gives the enzyme a
charter RM(xylose)/Km(glucose) ratio compared with the wild type.

The GI is used in industrial processes, e.g. for the prodn. of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FGASDTEREAHVKRFRQALDATGMTVPMATTNLFTHPVFKAGAFTANDRAVRRYALRKTI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RNIDLAVELGAKVYVAWGGREGAESGAAKDVRAALDRMKEAFDLLGEYVTSQGYDIRFAI 179
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م
                                                                                                                                                                                                                                                                                                                                                                                     66.5%; Score 1348.5; DB 1; Length 394; 65.5%; Pred. No. 3.2e-119; ive 50; Mismatches 77; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-AUG-1990 (first entry)
Amino acid sequence of Actinoplanes missouriensis (DSN 43046)
D-glucose isomerase (EcoAmi(DSM) GI)
Actinoplanes missouriensis (DSM 43046); D-glucose isomerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RTAYEDFDVDA-AARGMAFERLDQLAMDHLLGAR 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= mutation
/note=" Ala -> Lys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R05282 standard; protein; 394
             'label- helix
                                                                                                                                                                                                                                                                                                                             high fructose corn syrup.
See also R13278-R13287.
  .327
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                                                                       07-AUG-1991.
02-JAN-1991; 200003
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Best Local Similarity
Matches 258; Conserv
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Biologically active modified protein prodn. -
comprises substituting arganine residue for lysine in starting protein
Disclosure; Fig 15: 64pp; English.
It is D-glucose isomerase from Actinoplanes missouriensis
(DSM 43046). Its DNA is genelically engineered to code for a mutein
that has increased thermostability and increased resistance
the chemical modification. Its DNA is used in an example of
the method, which is claimed, where one or more Lys are substd. by Arg o
vice versa, at a site which can accommodate such a substitution without
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 FGASDTEREAHVKRFRQALDATGMTVPMATTNLFTHPVFKAGAFTANDRAVRRYALRKTI 119
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                                                                            17-JUL-1989; 201893.
17-JUL-1989; EP-201893, EP-201539.
(KONN) Gist-Brocades NV (PLAN').
Mrabet N. Lasters I, Stanssens P, Mathyssens G,
WPI, 90-052789/08.
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Glucose isomerase mutant T90s.
GI; high fructose corn syrup; sweetener; sugar.
isomerase; D-xylose.ketol-isomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RTAYEDFDVDA-AARGMAFERLDQLAMDHLLGAR 385
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132. 137
/label beta_strand
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/label- beta_strand
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|abel= beta_strand
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         Actinoplanes missouriensis. EP355039-A.
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Best Local Similarity 65.28
Matches 257; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EPKPNEPRGDILLPTIGHALAFIERLERPELYGVNPEVGHEQMAGLNFPHGIAQALWAGK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LEHIDLNGGSGIKYDQDLRFGAGDLRAAFWLVDLLESA----GWEGPRHFDFKPPRTED 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MNYOPTPEDRFTFGLWTVGWQGRDPFGDATRPALDPVD-VQRLAELGAYGVTFHDDDLIP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P. 07-406-1991.

P. 02-JAN-1991; 200003.

R. 02-JAN-1991; EP-200029.

R. 02-JAN-1991; EP-200029.

A. (PLAN-) PLANT GENETIC SYST NV.

A. (PLAN-) PLANT GENETIC SYST NV.

A. (PLAN-) PLANT GENETIC SYST NV.

Glucose isomerase mutants with altered substrate specificity - and mothods for selecting aminoacid(s) for substitution, used of . in prodn. of high fructose corn syrup.

T. e.g. in prodn. of high fructose corn syrup.

T. e.g. in prodn. of night fructose corn syrup.

C. claim 13; Page 13; 18pp; English.

T. e. substitution, used a better km(xylose)/Km(glucose) ratio than the wild type.

T. d. in industrial processes, e.g. for the prodn. of See also R13278 R13287.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66.3%; Score 1345.5; DB 1; Length 394; 65.2%; Pred. No. 6.2e-119; 1ve 51; Mismatches 77; Indels 9;
                             /label beta_strand
241. 246
241. 246
289. .292
/label beta_strand
32. 47
3. 47
3. 48
4. .83
/label helix
108. .130
/label helix
                                                                                                                                                                                      127. .239

/label- helix

264. .276

300. .327

/label- helix

/label- helix

/label- mutation

/note- Glu -> Gln "
          il- beta_strand .218
                                                                                                                                               150. .173
/label= helix
                                                                                                                                                                  195. .204
/label= heltx
177. .181
/label= be
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Best Local Similarity 65.2%
Matches 257; Conservative
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RTAYEDFDVDA-AARGMAFERLDQLAMDHLLGAR 385
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Search completed: March 22, 2000, 23:43:24 Job time: 770 sec

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Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Fotal number

Database

Searched:

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STRAIN-SK;

BELGHITH-SRIH K.;

Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.

Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.

-!- CATALYTIC ACTIVITY: D-XXLOSE - D-XXLULOSE.

-!- COFACTOR: MAGNESIUM IS NECESSARY FOR THE ACTIVITY OF THE PROTEIN.

-!- SUBCELLULAR LOCATION: CYTOPLASMIC.

EMBL; Y15518; CAA75672.1; -:

PROSITE; PS00172; XXLOSE ISOMERASE 1; 1.

PROSITE; PS00173; XXLOSE ISOMERASE 1; 1.

PROSITE; PS00173; XXLOSE ISOMERASE 2; 1.

ISOMETASE; PENTOSE SHULT; XYLOSE metabolism; Magnesium.

SEQUENCE 386 AA; 42702 MW; 7837ACFI CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptomyces sp.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 100.0%; Pred. No. 2.5e-143;
Matches 386; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-WAY-1999 (TrEMBLrel. 10, Created)
01-WAY-1999 (TrEMBLrel. 10, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              386 AA
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009WXP7
009KXB9
005KXB9
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SEQUENCE FROM N.A.
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Q9ZAI3
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Q9xt3 ortra sativ
Q9xt3 ortra sativ
Q9xt3 ortra sativ
Q9x0 thermotoga
Q9xb3 streptomyce
Q9420 streptomyce
Q9420 methanobact
Q17899 caenorhabdi
C17899 caenorhabdi
C1666 amycolatops
Q9zqa4 streptomyce
Q9zq0 streptomyce
Q5x60 streptomyce
Q5x60 streptomyce
Q5x60 streptomyce
Q5x60 streptomyce
Q1303 homo sapien
Q13303 homo sapien
Q9xnh0 salmonella
                                                                                                                              (without alignments) 680.472 Million cell updates/sec
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P77995 thermoanaer
09x422 lactococcus
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                                                                                                              March 22, 2000, 23:43:59; Search time 39.33 Seconds
                                Compugen Ltd
                                                                                                                                                                                                                                                                                                                             hits satisfying chosen parameters:
                 GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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Listing first 45 summaries
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A HAFT D.H., HICKEY E.K., PETERSON J.D., NELSON W.C., KETCHUM K.A.,
A MCDONALD L., UTTERBACK T.R., MALEK J.A., LINHER K.D., GARRETT M.M.,
STEWART A.M., COTTON M.D., PRATT M.S., PHILLIPS C.A., RICHARDSON D.,
A HEIDELBERG J., SUTTON G.G., FLEISCHHANN R.D., WHITE O., SALZBERG S.L.,
SMITH H.O., VENTER J.C., FRASER C.M.;
SMITH H.O., VENTER J.C., PRASER C.M.;
SMITH H.O., VENTER J.C., PRASER C.M.;
C. -I- CATALYTIC ACTIVITY: D-XYLOSE = D-XYLULOSE.
C. -I- CATALYTIC ACTIVITY: D-XYLOSE = D-XYLULOSE.
C. -I- CATALYTIC ACTIVITY: D-XYLOSE = D-XYLULOSE.
C. -I- SUBCELLULAR LOCATION: CYTOPLASMIC.
RMBL; ACOTOR: MAGNESUM IS NECESSARY FOR THE ACTIVITY OF THE PROTEIN.
C. -I- SUBCELLULAR LOCATION: CYTOPLASMIC.
RMBL; ACOTOR: MAGNESUM: SYLOSE_ISOMERASE_1; 1.
R PROSITE: PSOU172; XYLOSE_ISOMERASE_1; 1.
R PROSITE: PSOU172; XYLOSE_ISOMERASE_2; 1.
R PROSITE: PSOU173; XYLOSE_ISOMERASE_2; 1.
R ISOMERASE; PENTOSE SHURT; XYLOSE_ISOMERASE_2; 1.
R ISOMERASE; PENTOSE SHURT; XYLOSE_ISOMERASE_2; 1.
R SEQUENCE 444 AA; 50835 MM; 7DEEGCB2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDGINE; 99287316.
MELSON K.E., CLATTON R.A., GILL S.R., GWINN M.L., DODSON R.J.,
HAFT D.H., HICKEY E.K., PETERSON J.D., NELSON W.C., KETCHOM K.A.,
MCDONALD L., UTTERBACK T.R., MALEK J.A., LINHER K.D., GARRETT M.M.,
STEWART A.M., COTTON M.D., PRATT M.S., PHILLIPS C.A., RICHARDSON D.,
HEIDELBERG J., SUTTON G.G., FLEISCHMANN R.D., WHITE O., SALZBERG S.L.,
SWITH H.O., VENTER J.C., FRASER C.M.;
"Evidence for leteral gene transfer between Archaea and Dacteria from
Nature 399:323-329(1999).
                                                                                                                                         300
                                                                                                                                                                                                                   SAAGCMRNYLILKERAAAFRADPEVQEALRAARLDQLAEFTAADGLQALLADRTAYEDFD 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DDLIPFGASDTEREAH-----VKRFRQALDATGMTVPMATTNLFTHPVFKAGAFTANDR 108
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                                                                                                                                                                                                                                                  PKPNEPRGDILLPTIGHALAFIERLERPELYGVNPEVGHEQMAGLNFPHGIAQALWAGKL
                                                                                                         FHIDLNGQSGIKYDQDLRFGAGDLRAAFWLVDLLESAGWEGPRHFDFKPPRTEDIDGVWA
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28.1%; Pred. No. 5.9e-16;
.ive 67; Mismatches 177; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
XYLOSE ISOMERASE (EC 5.3.1.5).
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Matches 115; Conservative
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09X1Z5;
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281 HELRMARILGKLGSIDANQGDLLLGWDTD-QFPINIYDTTLAMYEVIKAGGFTKGGLNFD 339
                                                                                                                                                                                                                                                                                                                                                            340 AKVRRASYKVEDLFIGHIAGMDTFALGFKIAYKLAKDGV----FDKFIEEKYRSFKEGIG 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DDLIPFGASDTEREAH-----VKRFRQALDATGMTVPMATTNLFTHPVFKAGAFTANDR 108
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                                                                              TSQGYDIRFALEPKPNEPRGDILLPTIGHALAFIERLERPELYGVNPEVGHEQMAGLNFP
                                                                                                                                  KKIGFTGQFLIEPKPKEPTKHQYDFDVATAYAFLKNHGLDEYFKFNIEANHATLAGHTFQ
                                                                                                                                                                                            HGIAQALWAGKLFHIDLN-GOSGIKYDQDLRFGAGDLRAAFWLVDLLESAGW-EGPRHFD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                KEIVEGKIDFEKLEEYIIDK ---EDIELPSGKQ----EYLESILNSYIV 437
                                                                                                                                                                                                                                                                                                                                                                                                                   334 LDQLAEPTAADGLQALLADRTAYEDFDVDAAARGMAFERLDQLAMDHLL 382
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-1- CATALYTIC ACTIVITY: D-XYLOSE = D-XYLUIOSE.
-1- CORACTOR: MAGNESIUM IS NECESSARY FOR THE ACTIVITY (CORACION: USUBCELLULAR LOCATION: CYTOPLASMIC.
EMBL; U21678; AAC44473.1; -1- SUBCELLIAR PROCESTE; PS00172; XXLOSE_ISOMERASE_1; 1.
PROSITE; PS00173; XXLOSE_ISOMERASE_2; 1.
PROSITE; PR00688; XXLOSE_ISOMERASE_2; 1.
PRINTS; PR00688; XXLOSISHRASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isomerase; Pentose shunt; Xylose metabolism; Magnesium
SEQUENCE 439 AA; 50342 MW; 14C5E45C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01.FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thermoanaerobacterium SP.
Bacteria: Firmicutes; Bacillus/Clostridium group;
Thermoanaerobacter group; Thermoanaerobacterium.
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Matches 108; Conservative
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MEDLINE; 96427326.
LIU S.Y., WIEGEL J
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Query Match
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                              | : | | | | | | | | | : | | : | | | | HELRYARINGVLGSIDANTGDMLLGWDTD-QFPTDIRMTTLAMYEVIKMGGFDKGGLNFD 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151 RAALDRMKEAFDLLGEYVTSQGYDIRFAIEPKPNEPRGDILLPTIGHALAFIERLERPEL 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              211 YGVNPEVGHEQMAGLNFPHGIAQALWAGKLFHIDLN-GQSGIKYDQDLRFG--AGDLRAA 267
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                                                                   ---IDGVWASAAGCMRNYLILKERAAAFRADPEVQEALRAARLDQL 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              322 MHQI-LLNGGLGKGGINFDAKVRRTSFKAEDL--ILAHIAG-MDTYARALKGAAAIIEDK 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 NYQP-----TPEDRFTFGL--W-TVGWQGRDPFGDATRPALDPVDVQ------ 41
                                                                                                                                                                                                                                                                                                                     Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                         H.-H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            203 GLEMDHMAKFFHLAIDYAKSINHLPIFLIEPKPKEPWTHQYDFDSATALAFLQKYDLDKY
             HGIAQALWAGKLFHIDLN-GQSGIKYDQDLRFGAGDLRAAFWLVDLLESAGWE-GPRHFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41 ----RLAE-LGAYGVTFHDDDLIPFGASDTEREAHVKRFRQAL----DATGMTVPMATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        263 FKLNLETNHAWLAGHTFEHELNTARTFNALGSIDANQGNYLLGWDTD-EFPTLVIDITLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54;
                                                                                                                                                                                                                                                                                                                                                                          SECUENCE FROM N.A.
STRAIN-NRRL B-4449;
STRAINSON X.A., PARK J.-H., DELAMARRE S.C., EL KHAL W., KAO
BASARAN P., BRYDGES S.D., BATT C.A.;
"The xylose and xylan loci of Lactococcus lactis.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF092042; AAD20255.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----PEVQEALRAARLDQLAEPTAADGLQALLADRTAY-EDFDVDA 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             378 FLSDIVDERYSSYKNTEVGQSIENGTAT-FESLAAFALEYGDDIELDS 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56; Mismatches 177; Indels
                                                                                            340 AKVRRASFEPEDLPLGHIAGMDSLAKGFKVAYKLVKDRV------
                                                                                                                                         383 IEERYA------SYKDGIGADIVSGKADFKSLEKYALEH 415
                                                                                                                       338 AEPTAADGLQALLADRTAYED-FDVDAAARGMAFERLDQLAMDH 380
                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 303; DB 2;
Pred. No. 6.4e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       439 AA; 49593 MW; 63A0D649 CRC32;
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                                                                                                                                                                                                                        439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.9%; Score 303; 29.7%; Pred. No. 6
                                                                                                                                                                                                                                                  Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 29.7% Matches 121; Conservative
                                                                                                                                                                                                                       PRELIMINARY;
                                                                  287 FKPPRT----ED
                                                                                                                                                                                                                                                                                         XYLOSE ISOMERASE
                                                                                                                                                                                                                                                                                                                                                  Lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isomerase.
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                                                                                                                                                                                                                       Q9X422
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RESULT 09X416

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83 VDAFFEJAEKLGVKYYCFHDIDJAPTGNSLKEFYANLDEITDHLLEKOKATGIKLLWNTA 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        268 FWLVDLLESAGWEGPRHFDFKPPRT----EDIDGVWASAAGCMRNYLILKERAAFRADP 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                            Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25 HYNPEEVVAGKIMEEQLHFALAFWHIIIMDGSDPFGGAIMER - PWDLEGGSELDRAHRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41 ----RLAE-LGAYGVTFHDDDLIPFGASDTEREAHVKRFRQAL----DATGMTVPMATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151 RAALDRMKEAFDLLGEYVTSQGYDIRFAIEPKPNEPRGDILLPTIGHALAFIERLERPEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           211 YGVNPEVGHEQMAGLNFPHGIAQALWAGKLFHIDLN-GQSGIKYDQDLRFG--AGDLRAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   322 MHQI-LLNGGLGKGGINFDAKVRRISFKAEDL--ILAHIAG-MDTYARALKGAAAIIEDK
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LIU J., YANG J.S.;
LSUD. Subtractive hybridization (SSH) identified candidate
Suppression subtractive hybridization (SSH) identified candidate
genes that are differentially expressed at rice young panicle.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 439;
                                                                                                                                                                                                                                                                                                          W., KAO
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                                                                                                                                                                                                                                                                                 STRAIN=210;
ERLANDSON K.A., PARK J.-H., DELAWARRE S.C., EL KHAL W.,
BASARAN P., BRYDGES S.D., BATT C.A.;
"The xylose and xylan loci of Lactococcus lactis.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF092040; AAD20243.1; -.
                                           Created)
Last sequence update)
Last annotation update)
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
XXLOSE ISOMERAE FRAGMENT).
Oryza sativa (Rice).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 14.8%; Score 300.5; DB 2; Local Similarity 29.0%; Pred. No. 9.8e-15; les 122; Conservative 57; Mismatches 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                439 AA; 49666 MW; FB50EDFD CRC32;
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PRT;
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                                         (TrEMBLrel. 12, (TrEMBLrel. 12, (TrEMBLrel. 12,
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PRELIMINARY;
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                XYLOSE ISOMERASE.
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                                         01-NOV-1999
01-NOV-1999
01-NOV-1999
                                                                                                                                                                                                             Lactococcus.
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SEQUENCE
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Isomerase.
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Matches
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MEDLINE; 99287316.
MEDLINE; 99287316.
MEDLINE; 99287316.
MELSON K.E., CLAYTON R.A., GILL S.R., GWINN M.L., DODSON R.J.,
MAFT D.H., HICKEY E.K., PETERSON J.D., NELSON W.C., KETCHUM K.A.,
MCDONALD L., UTTERBACK T.R., MALEK J.A., LINHER K.D., GARRETT M.M.,
STEWART A.M., COTTON M.D., PRATT M.S., PHILLIPS C.A., RICHARDSON D.,
HEIDELBERG J., SUTTON G.G., FLEISCHAMANN R.D., WHITE O., SALZBERG S.L.,
"EVIDENCE FOR INTER J.C., FRASER C.M.; WHITE O., SALZBERG S.L.,
"EVIDENCE OF INTER J.C., FRASER C.M.;
WEIGHORD SEQUENCE OF THE TRANSFER DETWEEN Archaea and bacteria from
Nature 399:323-329(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

NELSON K.B., CLAYTON R.A., GILL S.R., GWINN M.L., DODSON R.J.,

HAFT D.H., HICKEY E.K., PETERSON J.D., NELSON W.C., KETCHUM K.A.,

MCDONALD L., UTTERBACK T.R., MALEK J.A., LINHER K.D., GARRETT M.M.,

STEWART A.M., COTTON M.D., PRATT M.S., PHILLIPS C.A., RICHARDSON D.,

HEIDELBERG J., SUTTON G.G., FLEISCHMANN R.D., WHITE O., SALZBERG S.L.,

SMITH H.O., VENTER J.C., FRASER C.M.;

SUDMILLED (JUN-1999) to the EMBL/Genbank/DDBJ databases.

EMBL, AEOO1767; AAD36148.1; -.

ISOMATER 3.83 AA; 44732 MW; COC4EDE7 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EELREFAEEKGLKIGAINPNLFQDPDYKYGSLTNPSEKIRKKAIAHVMECVDIAEKTGSK 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     132 VYVAWGGREGAESGAAKDVRAALDRMKEAFDLLGEYVTSQGYDIRFAIEPKPNEP---RG 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 135 VISLWLA-DGTDYPGQDDFRSRKKRLEESLRYIYENMPA---DMYLLIEYKFFEPAFYHT 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72 KRFRQALDATGMTVPMATTNLFTHPVFKAGAFTANDRAVRRYALRKTIRNIDLAVELGAK 131
                                                                                                                                                                                                                                                                                            52 FHDDDLIPFGASDTEREAH----VKRFRQALDATGMTVPMATTNLFTHPVFKAGAFTAND 107
                                                                                                                                                                                                                                                                                                                                                                                       108 RAVRRYALRKTIRNIDLAVELGAKVYVAWGGREGAESGAAKDVRAALDRMKEAFDLLGEY 167
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                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                        27 FHDRDIAPDGKTLTETNKNLDEIVELAKKLQEETNIKPLWGTAQLFMHPRYMHGAATSPE 86
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                                                                                                                                                                                           Length 169;
                                                                                                                                                                                                                                             Indels
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Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF140230; AAD30135.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                             68;
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                                                                                                                                                                                           Query Match 8.7%; Score 176; DB 10; Best Local Similarity 30.2%; Pred. No. 4.5e-06; Matches 42; Conservative 25; Mismatches 68;
                                                                                                                         C04DD948 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      383 AA
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169 169
169 AA; 19511 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   168 VTSQGYDIRFAIEPKPNEP 186
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(TrEMBLrel. ]
(TrEMBLrel. ]
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Matches 76; Conserv
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SEEGER K., HARRIS D.;
"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-A3(2);
MEDILINE; 97000351.
REDENBACH M., FIESER H.M., DENAPAITE D., EICHNER A., CULLUM J.,
RENABHI H., HOPWOOD D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for
the 8 Mb Streptomycess coelicolor A3(2) chromosome.";
mol. Microbiol. 21:77-96(1996).
EMBL; AL096837; CAB48889.1; -.
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                                     62 ASD--TEREAHVKRFRQALDATGMTVPMATTNLFTHPVFKAGAFTANDRAVRRYALRKTI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 RNIDLAVELGAKVYVAWGGREGAESGAAKDVRAALDRMKEAFDLLGEYVTSQGYDIRFAI 179
DILLPTIGHALAFIERLERPELYGVNPEVGHEQMAGLNFPHGIAQALWAGKLFHIDLNGQ 248
                                                                                                                  SGIKYDQDLRFGAGDLRAAFWLVDLLESAGWEGPRHFDFKPPRTEDIDGVWASAAGCMRN 308
                                                                                                                                                                                                                                                                                                263 FLIFKEIVFAKR-DPELSDSAKKVVLMFDQAHITKPKILAMIQSVLIAQELFTKALLIDE 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 WTVGWQG------RDPFGDATRPALDPVDVQRLAEL--GAYGVTFHDDDLIPFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                        309 YLILKERAAAFRADPEVQEALRAARL--DQ--LAEPTAADGLQ-------ALLAD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                          ---KYADD-----DLTIA------SINPYEV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
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26.0%; Pred. No. 0.03;
1ve 39; Mismatches 160;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        386 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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01-NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PUTATIVE SUGAR ISOMERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                           353 ---RTAYEDFDV 361
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133 YVAWGGREGAESGAAKDVRAALDRMKEAFDLLGEYVTSQGYDIRFAIEPKPNEPRGDILL 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTIGHALAFIERLERPELYGVNPEVGHEQMAGLNFPHGIAQAL--WAGKLFHIDLNGQSG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              251 IKYDQDLRFGAGDLRAAFWLVDLLESAGWEG-----PRHFDFKPP-RTEDIDGVWASAA 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 ATGMTVPMATTNLFT-----HPVFKAGAFTANDRAVRRYALRKTIRNIDLAVELGAKV 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 GRDPFGDATRPALDPVDVQRLAELG--AYGVTFHDDDLIPFGASDTEREAHVKRFRQALD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces
                                                                               RTEDIDGVWASAAGCMRNYLILKERAAAFRADPEVQEALRAARLDQLAEPTA 342
                                                                                                                 | :: ||:|
---RINRSGEPSA 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REDENBACH M., KIESER H.M., DENAPAITE D., EICHNER A., CULLUM KINASHI H., HOPWOOD D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 5.9%; Score 120; DB 2; Length 290; Best Local Similarity 23.9%; Pred. No. 0.14; Matches 72; Conservative 48; Mismatches 133; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-A3(2);
BENTLEY S.D., PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SAUNDERS D.C., HARRIS D.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "A set of ordered commids and a detailed genetic and the 8 Mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996).
EMBL; AL035707; CAB38885.1; -.
                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                        290 AA
                                                                                                                                  ---RSLPFLRRAAPAPPPPP----
                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                290 AA; 31122 MW;
                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 10, TremBLrel. 10, TremBLrel. 10,
                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomyces coelicolor
                                                                                                                                                                                                                                                                                                                                                                                                          PUTATIVE ISOMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                              01-MAY-1999
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                                                                                                                                     284 YAE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G 304
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092420
AC 092420
AC 092420
DT 01-MAY
DT 01-MAX
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KINASHI H., HOPWOOD D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for
the 8 Mb Streptomycess coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL; AL023862; CAA19633.1; -
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                                                                               AGKLFHIDLNGQSGIKYDQDLRFGAGDLRAAFWLV-DLLESAGWEGPRHFDFKPPRTEDI 295
                                                                                                                                                                                     DGVWASAAGCMRNYLILKERAAAFRADPEVQEALRAARL---DQLAEPTAA-DGLQALLA 351
                                                                                                                                                                                                                                           ----AFMLDQCHNIEAKIPAIIRSVMNVQEATAKALLVDGTALAEAQAAGDVLEANAV 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIRNIDLAVELGAKVYVAWGGREGAESGAAKDVRAALDRMKEAFDLLGEYVTSQGYDIRF 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AIEPKPNEPRGDILLPTIGHALAFIERLERPELYGVNPEVGHEQMAGLNFPHGIAQALWA 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to the EMBL/GenBank/DDBJ databases
                                                                                                                 01-AUG-1998 (TIEMBLTE1. 07, Created) 01-AUG-1998 (TIEMBLTE1. 07, Last sequence update) 01-NOV-1998 (TIEMBLTE1. 08, Last annotation update) HYPOTHETICAL 33.5 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.2%; Score 125.5; DB 2;
4.4%; Pred. No. 0.062;
ve 46; Mismatches 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33543 MW; AB456D17 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             315 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 QGRDPFGDATRPALDPV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 6.2%;
Best Local Similarity 24.4%;
Matches 86; Conservative 4
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Submitted (JUN-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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MEDLINE; 97000351.
                                                                                                                                                                                                                                                                                              352 DRTAY 356
                                                                                                                                                                                                                                                                                                                                                       338
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SEQUENCE 31
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STRAIN-S699;
AUGUST P.R., TANG L., YOON Y.J., NING S., MUELLER R., HUTCHINSON C.R.,
FLOSS H.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Pseudonocardineae; Pseudonocardiaceae; Amycolatopsis.
                                                    83 MTVP----MATTNLFTH----PVFKA-----GAFTANDRAVRRYALRKT----IRNI 122
                                                                                                                              DLAVELGAK-----VYVAWGGREGAESGAAKDVRAALD-----RMKEAFDLLGEYVT 169
                                                                                                                                                  SQGYDIRFAIE------PKPNEPRGDILLPTIGHALAFIE-------R 204
                                                                                                                                                                                                                                     176 ENGVYLTFYAERVTWWLKVTAPGNP-----GHGSQFMENTAMEKIERFLASARAFR 226
                                                                                                                                                                                                                                                                           LERPELYGVNP--EVGHEQMAGLNFPHGIAQALWAGKLF--HIDLNGQSGIKYDQDLRFG 260
                                                                                                                                                                                                                                                                                                           227 NEGKELLEKNPTWALGDVTTLNVNILKGGVQFNVIPEKFEAYVDIR----LTPNQDF--- 280
                                                                                                                                                                                                                                                                                                                                                                     261 AGDLRAAF--WLVDLLESAGWEGPRHFDFKP--PRTEDIDGVWAS--------302
                  Indels 102; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-S699;
AUGUST P.R., TANG L., YOON Y.J., NING S., MUELLER R., YU T.W.,
TAYLOR M., HOFFMANN D., KIM C.G., ZHANG X., HUTCHINSON C.R.,
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SEQUENCE FROM N.A.
STRAIN-LBG A3136;
SCHOLP I., TOUPET C., ENGEL N., GOFF S.;
SUBMITTED TO TOUPET C., ENGEL N., GOFF S.;
SUBMIT A213012;
EMBL, A223012;
EMBL, A223012;
EMBL, A223012;
EMBL, A223012;
EMBL, A223012;
EMBL, A223012;
EMBL, A203013;
EMBL, A20006;
EMBL, AMPBINDING.
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KIM C.G., YU T.W., FRYHLE C., HANDA S., FLOSS H.G.;
J. Biol. Chem. 0:0-0(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
Pred. No. 2.9;
46; Mismatches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 4735 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                      302 -AAGCMRNYLILKERAAAFRADPEVQEALRA 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                        338 VCVGSTDSRFVRKAGVPAINFSPMINTPVRA 368
Similarity 20.5%;
8; Conservative 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Amycolatopsis mediterranei.
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Chem. Biol. 5:0-0(0002).
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 Best Local Sim
Matches 68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    156 AEELG - VMVTLDAAHAATMGYSTEEMVSAHVGHVHLSDNTGEVDSHDALGEGSLDFQA- 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96 PVFKAGAFTANDRAVRYALRKTIRNIDLAVELGAKVYVAWGGREGAESGAAKDVRAALD 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   214 NPEVGHEQMAGLNFPHGI ----AQALWAGKLFHIDLNGQSGIKYDQD-LRFGAGDLRAA 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TIEMBLIE). 01, Created)
01-NAY-1999 (TIEMBLIE). 10, Last sequence update)
01-NOV-1999 (TIEMBLIE). 12, Last annotation update)
01-NOV-1999 (TIEMBLIE). 12, Last annotation update)
01-005.4.
C1005.4.
C2005.4.
Canorhabitis elegans.
Eukaryota; Metazoa; Menatoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                  01-3A1-1998 (TrEMBLrel. 05, Created)
01-3AN-1998 (TrEMBLrel. 05, Last sequence update)
01-3AN-1998 (TrEMBLrel. 05, Last annotation update)
01-ANG-1998 (TrEMBLrel. 07, Last annotation update)
CONSERVED PROTEIN.
MTH2A7.
Archaea; Euryarichaeota; Methanobacteriales; Methanobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 5.3%; Score 107; DB 1; Length 233; Local Similarity 26.6%; Pred. No. 0.96; es 54; Conservative 32; Mismatches 83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases EMBL, Z68114; CAA92447.1; -. PFAN: PFO1546; Peptidase_M20; 1. SEQUENCE 397 AA; 45242 MW; 0963D445 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    233 AA; 25067 MW; F9D4C1C3 CRC32;
                                     233 AA
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                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           213 -- LLDGLRGAGYTGVLTVEVKTP 233
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                                     PRELIMINARY;
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Query Match

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----TINLFIH-----PVFKAGAFTANDR----AVRRYALRKTIRNIDLAVELG
                                                                                                                                                                                                                                                                                                                                         373 A.A.
                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                           3513 VDEAWLDRPADAA 3525
                                                                                                                                                                                                                                                   352 DRTAYEDFDVDAA 364
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nes 72; Conservat
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85 VPMA
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                                                                        22;
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                                                                                                                                                                                                                       4516 -AVADMDWAARIPARTSV----RPSPLFADLPEAKAILRAAQDDGED-----GDTASSLA 4565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3203 PAAPAPLPAADPVP----AGRLTALT 3242
                                                                                                                  :| : : ||| : : ||| 4566 DSLRAV----PDAEQURILLXLVRGHASTV----LGHSGAEGIGPRQAFQEVGFDSLAAVN 4618
                                                                                                                                                                                                                                                                                                                                                                             4660 GLDG------REDDLRRVLAAVPFARFKEAGVLDTLLGLADTGTEPGTDAETTEAAP 4710
                                                                                                                                                   LIPFGASDTEREAHVKRFRQALDATGMTVPMATTNLFTHPVFKAGAFTANDRAVRYALR 116
                                                                                                                                                                                                                                                                                                    227 FPHGIAQALWAGKLFHIDLNGQSGIKYDQDLRFG-----AGDLRAAFWLVDLLESA-- 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84
                                                                                                 3 YQPTPEDRFTF----GLWTVGWQGRDPFGDATRPALDP-VDVQRLAELGAYGVTFHDDD
                                                                                                                                                                                                  117 KTIRNIDLAVELGAKVYVAWGGREG---AESGAAKDV-RAALDRMKEAFDLLGEYVTSQG
                                                                                                                                                                                                                                                                                                                             4619 LRN------VELLREADD
                                                                                                                                                                                                                                                                                                                                                      278 GWEGPRHFDFKPPRTEDIDGVWASA-----AGCMRNYLILKERAAAFRADPEVQEALR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
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                                                                                                                                                                          4474 QIGIGMD----EAALAQLRRR-GVIPMAPPLAVTAM-----VQAVAGNEKAV----
                                                                                                                                                                                                                                                    173 YDIRFAIEPKPNEPRGDILLPTI-GHALAFIERLERPELYGVNP----EVGHEQMAGLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-MA6548;
MEDLINE; 98451508.
MOTAMEDH H., SHAFIEE A.;
The blosynthetic gene cluster for the macrolactone ring of the immunosuppressant FK506.";
Eur. J. Blochem. 256:528-534(1998).
EMBL; AF082100; ARC68815.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 7576;
                                               Query Match 5.2%; Score 105; DB 2; Length 4735; Best Local Similarity 24.5%; Pred. No. 1.1e+02; Matches 92; Conservative 46; Mismatches 140; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 5.0%; Score 100.5; DB 2; Best Local Similarity 24.7%; Pred. No. 4.5e+02; Matches 92; Conservative 31; Mismatches 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42E87D19 CRC32,
             FC634DAE CRC32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7576 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS00455; AMP_BINDING; 1.
PS00606; B_KETOACYL_SYNTHASE; 4.
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              495213 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                             4711 AADDAELIDALDISGL 4726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FK506 POLYKETIDE SYNTHASE.
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           4735 AA;
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Transferase.
SEQUENCE 4
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01-MAY-1999
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01-NOV-1999
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Transferase
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MEDLINE; 97000351.
REDEMBACH M., KIESER H.M., DENAPAITE D., EICHNER A., CULLUM J.,
KINASHI H., HOPWOOD D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL, A1033505; CAA22050.1; -.
Hypothetical protein.
SEQUENCE 373 AA; 40702 MW; AEA38C6C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93 FTHPVFK-----AGAFTANDRAVRRYALRKTIRNIDLAVELGAKVYVAWGGREGAESGAA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         148 KDVRAALDRMKEAFDLLGEYVTSQGYDIRFAIEPKPNEPRGDILLPTIGHALAFIERLER 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 FLHPLYEHQGPWASVYVDLSRHTEDTPHERELTAAAVAREL-----AEQGADDATC 55
                                                                                                                 :: | | | | | | | : | | : | | : | | SQ----WDGM-GAELLATEPVFAR--RIGECAEALAPYT---GWDLLDVIARRPGAPELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCIEG. 22C.
Streptomyces coellcolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomyclneae; Streptomyces.
3243 APAAAIGHSLATTRTAMRHRAVVPARDAEAFARGEEVPGVVRGTADVTDTRAVFVFPGQG
                                                                      130 AKVYVAWGGREGAESGAAKDVRAALDRMKEAFDLLGEYVTSQGYDIRFAIEPKPNEP---
                                                                                                                                                                                                         RGDILLPTIGHALAFIERLERPELYGVNPE--VGHEQ------MAG-LNFPHGIAQALW
                                                                                                                                                                                                                                                                                                                                            237 AGKLFHIDLNGQSGIKYDQDLRFGAGDLRAAFWLVDLLESAGWEGPRHFDFKPPRTEDID
                                                                                                                                                                                                                                                                                                                                                                                                        3411 RSRLVATERAGHGGM-----VSVPPADFDAAAW-AGRLEVAAVNGPASI------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GVWASAAGCMRNYLILKERAAAFRADPEVQ----EALRAARLDQLAEPT-AADGLQALLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-A3(2);
SEEGER K.J., HARRIS D.;
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
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PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1999 (TrEMBLrel. 10, Created)
(1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
HYPOTHETICAL 40.7 KD PROTEIN
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22.4%; Pred. No. 10;
tive 29; Mismatches 108;
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Search completed: March 22, 2000, 23:47:30 Job time: 211 sec

protein

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Run on:

Sequence:

Title: Perfect

Minimum DB Maximum DB

Searched:

Database :

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rhizobium f
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saccharopol
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PDB; 2GYI; 10-JUL-95.
PROSITE; PSO0172; XYLOSE_ISOMERASE_1; 1.
PROSITE; PSO0173; XXLOSE_ISOMERASE_2; 1.
PFAM; PF00259; Xylose_isom; 1.
Isomerase; Pentose shunt; Xylose metabolism; Magnesium; 3D-structure.
INIT_MET
ACT_SITE 53 53 BY SIMILARITY.
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SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (1.81 ANGSTROMS).
MEDLINE; 94235606.
LAVIE A., ALLEN K., PETSKO G.A., RINGE D.;
"X-ray crystallographic structures of D-xylose isomerase-substrate complexes position the substrate and provide evidence for metal movement during catalysis.";
Biochemistry 33:5469-5480(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
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MEDLINE; 90057422.
MEDLINE; R., GLASFELD A., TIRABY G., RINGE D., PETSKO G.A.;
"Crystallographic studies of the mechanism of xylose isomerase.";
Biochemistry 28:7289-7297(1989).
P12255
Q00105
P09239
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P22523
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Bacteria, Firmicutes, Actinob
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                  GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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XYLA_HORVU
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Listing first 45 summaries
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                                                                                                                                                                                  Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                             Streptomyces
                                                                                 01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
XXLOSE ISOMERASE (EC 5.3.1.5).
                             388 AA
STANDARD;
                                                                Streptomyces murinus.
                            XYLA_STRMR
P37031;
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94.4%; Score 1916; DB 1;
Best Local Similarity 94.3%; Pred. No. 6.1e-143;
Matches 364; Conservative 13; Mismatches 7;
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                         [1]
SEQUENCE FROM N.A., AND SEQUENCE OF 1-20.
STRAIN=CBS 409-73;
MEDLINE; 89016633.
DROCOURT D., BEJAR S., CALMELS T., REYNES J.-P., TIRABY G.;
"Nucleotide sequence of the xylose isomerase gene from Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 NYOPTPEDRFTFGLWTVGWQGRDPFGDATRPALDPVD-VQRLAELGAYGVTFHDDDLIPF
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces
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15; Mismatches 12; Indels
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MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
                                                                                                                      -i - FUNCTION: INVOLVED IN D-XYLOSE CATABOLISM.
-i - CATALYTIC ACTIVITY: D-XYLOSE = D-XYLULOSE.
-i - COFACTOR: MAGNESIUM IS NECESSARY FOR THE ACTIVITY.
-i - SUBGNIT: HOMOFETRAMER.
-i - SUBCELLULAR LOCATION: CYTOPLASMIC.
-i - SIMILARITY: BELONGS TO THE XYLOSE ISOMERASE FAMILY.
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EMBL; M36269; AAA26839.1; -.
PIR; S01436; ISSMXV.
HSSP; P37031; 1DXI.
PROSTIE; PS00172; XXLOSE_ISOMERASE_1; 1.
PROSTIE; PS00173; XXLOSE_ISOMERASE_2; 1.
PFAM; PF00259; Xylose_1som; 1.
                                                                                                violaceoniger.";
Nucleic Acids Res. 16:9337-9337(1988)
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Matches 358; Conservative
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93.6%; Score 1900; DB 1;
Best Local Similarity 92.8%; Pred. No. 1.1e-141;
Matches 360; Conservative 14; Mismatches 12;
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388 AA;
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61 GASDTEREAHVKRFRQALDATGMTVPMATTNLFTHPVFKAGAFTANDRAVRRYALRKTIR 120
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llarity 92.2%; Pred. No. 1.7e-139;
Conservative 14; Mismatches 14;
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387 AA;
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R PIR; B41339; B41339;
R PDB; IXIS; 15-JUL-92.
R PDB; 3XIS; 15-JUL-92.
R PDB; 3XIS; 15-JUL-92.
R PDB; 3XIS; 15-JUL-92.
R PDB; 1XID; 22-JUN-94.
R PDB; 1XID; 22-JUN-94.
R PDB; 1XIS; 22-JUN-94.
R PDB; 1XII; 22-JUN-94.
R PDB; 1
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CARRELL H.L., GLUSKER J.P., BURGER V., MANFRE F., TRITSCH D., BIELLMANN J.-F.; GLUSKER J.P., BURGER V., MANFRE F., TRITSCH D., BIELLMANN J.-F.; GLUSKER J.P., BURGER V., MANFRE F., TRITSCH D., BIELLMANN J.-F.; GLUSKER J.P., BURGER V., MALLS GRANDLISM designed inactivator."; Toomplex with substrate and with a mechanism-designed inactivator."; Proc. Natl. Acad. Sci. U.S.A. 86:440-444(1989).

C. I. CATALYTIC ACTIVITY: D.YXLOSE CATABOLISM.

C. I. CATALYTIC ACTIVITY: D.YXLOSE D. D.XXLULOSE.

C. I. CATALYTIC ACTIVITY: D.YXLOSE D.YXLULOSE.

C. I. SUBGLICHTAR LOCATION: CYTOPLASMIC.

C. I. SUBCLILIARITY: BELONGS TO THE XYLOSE ISOMERASE FAMILY.

C. I. CAUTION: ACCORDING TO THE CRYSTALLOGRAPHIC STUDY RESIDUE 40

COULD BE GLN.
                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 92041569.
MEDLINE; 92041569.
WOOG H.C., TING Y., LIN H.C., REICHERT F., MYAMBO K., WATT K.W.,
TOY P.L., DRUMMOND R.J.;
"Genetic organization and regulation of the xylose degradation genes
in Streptomyces rubiginosus.";
J. Bacteriol. 173:6849-6858(1991).
                                                                                                                                                                                                                                                                                          Streptomyces rubiginosus.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
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MAGNESIUM (BY SIMILARITY).
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01-APR-1993 (Rel. 25, Last sequence update)
12-UL-1999 (Rel. 38, Last annotation update)
XYLOSE ISOMERASE (EC 5.3.1.5).
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                                                                NIDLAVELGAKVYVAWGGREGAESGAAKDVRAALDRMKEAFDLLGEYVTSQGYDIRFAIE
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MEDLINE; 91197439.

DAUTER Z., TERRY H., WITZEL H., WILSON K.S.;
FRÉILDEMENT OF GLUCOSE ISONGERSE From Streptomyces albus at 1.65
with data from an imaging plate.";
Acta Crystallogr. B 46:833-845(1990).
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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01-WAR-1992 (Rel. 21, Last sequence update)
01-LUL-1999 (Rel. 38, Last annotation update)
XYLOSE ISOMERASE (EC 5.3.1.5).
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61 GSSDSERYEHVKRFRQALDDTGMKVPWATTNLFTHPVFKDGGFTANDRDVRRYALRKTIR 120
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91.7%; Pred. No. 8.7e-139;
ive 15; Mismatches 15;
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55; Conservative
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ASAAGCMRNYLILKERAARFRADPEVQEALRAARLDQLAEPTAADGLQALLADRTAYEDF 359
                                                                                  RNIDLAVELGAKVYVAWGGREGAESGAAKDVRAALDRMKEAFDLLGEYVTSQGYDIRFAI 179
                                                                                                                                                                                                                       LFHIDLNGQSGIKYDQDLRFGAGDLRAAFWLVDLLESAGWEGPRHFDFKPPRTEDIDGVW 299
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KIKUCHI T., ITOH Y., KASUMI T., FUKAZAWA C.;
"Molecular cloning of the xylA gene encoding xylose isomerase from
Streptomyces griseofuscus S-41: primary structure of the gene and its
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
  EPKPNEPRGDILLPTIGHALAFIERLERPELYGVNPEVGHEQMAGLNFPHGIAQALWAGK
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01-AUG-1991 (Rel. 19, Last sequence update)
15-JUC-1999 (Rel. 38, Last annotation update)
XYLOSE ISOMERASE (EC 5.3.1.5).
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KX PELINE, 95101954.

KWANG Y., HUANG Z., DAI X., LIU J., CUI T., NIU L., WANG C., XU X.;

WANG Y., HUANG Z.,

"The sequence of xylose isomerase gene from Streptomyces diastaticus

"The sequence of xylose isomerase gene from Streptomyces diastaticus

"The sequence of xylose isomerase gene from Streptomyces diastaticus

"The sequence of xylose isomerase gene from Streptomyces diastaticus

"The sequence of xylose isomerase gene from Streptomyces diastaticus

"The sequence of xylose isomerase gene from Streptomyces diastaticus

"The sequence of xylose isomerase controls."

"I Chin. J. BONGTENTY INVOLUTY: D. XYLOSE D. D. XYLUGOSE.

"I COPACION: MAGNESIUM IS NECESSARY FOR THE ACTIVITY."

"I SUBUNTY: HONOTETRAMER (BY SIMILARITY).

"I SUBCELLULAR LOCATION: CYTOPLASMIC."

"I SIMILARITY: BELONGS TO THE XYLOSE ISOMERASE FAMILY."
                                                                                                                                                                                             SAAGCMRNYLILKERAAAFRADPEVQEALRAARLDQLAEPTAADGLQALLADRTAYEDFD 360
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PKPNEPRGDILLPTVGHALAFIERLERPELYGVNPEVGHEQMAGLNFPHGIAQALWAGKL
                                                                                  PHIDLNGQSGIKYDQDLRFGAGDLRAAFWLVDLLESAGWEGPRHFDFKPPRTEDIDGVWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces
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PROSITE: PS00173; XYLOSE_ISOMERASE_2; 1.
PFMA: PF00259; XYLOSE_ISOME: 1.
ISOMerase; Pentose shunt; Xylose metabolism; Magnesium.
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89.9%; Pred. No. 1.6e-136;
1ve 16; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            XYLA_STRDI STANDARD; PRT; 388 AA. P50910; 01-0cT-1996 (Rel. 34, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) XYLOSE ISOMERASE (EC 5.3.1.5).
                                                                                                                                                                                                                                                                       361 VD-AAARGMAFERLDQLAMDHLLGARG 386
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Best Local Similarity
Matches 349; Conserv
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SEQUENCE
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                                                    GASDTEREAHVKRFRQALDATGMTVPMATTNLFTHPVFKAGAFTANDRAVRRYALRKTIR 120
                  NIDLAVELGAKVYVAWGGREGAESGAAKDVRAALDRMKEAFDLLGEYVTSQGYDIRFAIE 180
                                                                                                                                                       VWASAAGCMRNYLILKE-------RAAAFRADPEVQEALRAARLDQLAEPTAAD 344
                                                                                                                                                                                                                                                                                                                                                                                                  AMORE R., HOLLENBERG C.P.;
"XyJose isomerase from Actinoplanes missouriensis: primary structure
of the gene and the protein.";
Nucleic Acids Res. 17:7515-7515(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Protein engineering of xylose (glucose) isomerase from Actinoplanes missouriensis. 1. Crystallography and site-directed mutagenesis of metal binding sites.";
                                                                               PKPNEPRGDILLPTIGHALAFIERLERPELYGVNPEVGHEQMAGLNFPHGIAQALWAGKL
                                                                                                                   FHIDLNGQSGIKYDQDL---RFGAGDLRAAFWLVDLLESAGWEGPRHFDFKPPRTEDIDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 89184498.

REY F., JENKINS J., JANIN J., LASTERS I., ALARD P., CLAESSENS M., MATTHYSSENS G., WODAK S.G.;

"Structural analysis of the 2.8 A model of Xylose isomerase from Actinoplanes missouriensis.";

Proteins 4:165-172(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JENKINS J., JANIN J., REY F., CHIADMI M., VAN TILBEURGH H.,
LASTERS I., DE MAEYER M., VAN BELLE D., WODAK S.J., LAUWEREYS
STANSSENS P., MRABET N.T., SNAUWAERT J., MATTHYSSENS G.,
                                                                                                                                                                                                                                                                                                                                            Actinomycetales; Micromonosporineae; Micromonosporaceae; Actinoplanes.
                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                            01-0cT-1989 (Rel. 12, Created)
10-0cT-1993 (Rel. 27, Last sequence update)
10-UL-1999 (Rel. 38, Last annotation update)
XYLOSE ISOMERASE (EC 5.3.1.5).
                                                                                                                                                                                                                                                           393 AA
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RAMIN M., SHEPARD W., FOURME R., KAHN R.;
Submitted (JUN-1998) to the PDB data bank.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
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                                                                                                                                                                                                      345 GLQALLADRTAYEDFDVD-AAARGM 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochemistry 31:5449-5458(1992).
                                                                                                                                                                                                                                                                                                                          Actinoplanes missouriensis.
                                                                                                                                                                                                                                                           STANDARD;
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MEDLINE; 92304916.
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MEDLINE; 90016811
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                                                                                                                                    AMURADEN SIS.

RA VAN TILBBURGH H., JENKINS J., CHIADMI M., JANIN J., WODAK S.J.,

RA VAN TILBBURGH A.-M.;

RA MRABET N.T., LAMBEIR A.-M.;

RA MRABET N.T., LAMBEIR A.-M.;

RI Sibe-directed mutageness.";

RI Site-directed mutageness.";

RI Site-directed mutageness.";

RI Site-directed mutageness.";

C. -! CATALYIT ACTIVIT: D-XYLOSE = D-XYLULOSE.

C. -! CATALYIT ACTIVIT: D-XYLOSE = D-XYLULOSE.

C. -! COFACTOR: MAGNESIUM IS NECESSARY FOR THE ACTIVITY.

C. -! SUBCELLULAR LOCATION: CYTOPLASMIC.

C. -! SUBCELLULAR LOCATION: CYTOPLASMIC.

C. -! SIMILARITY: BELONGS TO THE XYLOSE ISOMERASE FAMILY.

C. -! SIMILARITY: BELONGS TO THE XYLOSE ISOMERASE FAMILY.
LAMBEIR A.-M., LAUWEREXS M., STANSSENS P., MRABET N.T., SNAUWAERT J., VAN TILBEURGH H., MATTHYSSENS G., LASTERS I., DE MAEYER M., WODAK S.J., JENKINS J., CHIADMI M., JANIN D.; Protein engineering of xylose (glucose) isomerase from Actinoplanes missouriensis. 2. Site-directed mutagenesis of the xylose binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xylose metabolism; Magnesium; 3D-structure.
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POSSITE; PSO0173; XXLOSE_ISOMERASE_1; 1.

PROSITE: PSO0173; XYLOSE_ISOMERASE_2; 1.

PFAM; PF00259; Xylose_1som; 1.
                                                                                                            Biochemistry 31:5459-5466(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X16042; CAA34164.1; -. EMBL; A10241; CAA00884.1; -.
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8XIM; 15-JUL-93.
9XIM; 15-JUL-93.
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2XIM; 15-APR-93.
3XIM; 15-APR-93.
4XIM; 15-JUL-93.
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2XIN; 15-JUL-93.
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5XIN; 15-JUL-93.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . P.J.;
for xylose
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303 VWESAKANIRMYLLLKERAKAFRADPEVQEALAASKVAELKTPTLNPGEGYAELLADRSA 362
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llarity 65.7%; Pred. No. 3.4e-98;
Conservative 46; Mismatches 80; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAARI G.C., KUMAR A.A., KAWASAKI G.H., INSLEY M.Y., O'HARA "Sequence of the Ampullariella sp. strain 3876 gene coding
                                                                                                                                                                                                                                                                                                                                                                                Bacteria, Firmicutes, Actinobacteria, Actinobacteridae, Actinomycetales, Micromonosporineae, Actinoplanes.
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-1- SUBCELLULAR LOCATION: CYTOPLASMIC.
-1- SIMILARITY: BELONGS TO THE XYLOSE ISOMERASE FAMILY.
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PROSITE; PS00173; XYLOSE_ISOMERASE_2; 1.
PFAM, PF00259; XYLOSE_LSOM; 1.
ISOMERASE; Pentose shunt; Xylose metabolism; Magnesium.
ACT_SITE 54 54 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Bacteriol, 169:612-618(1987).
--- CATALYTIC ACTIVITY: D-XYLOSE - D-XYLULOSE.
--- COFACTOR: MAGNESIUM IS NECESSARY FOR THE ACTIVITY.
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01-JUL-1989 (Rel. 11, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
XYLOSE ISOMERASE (EC 5.3.1.5).
                                                                                                                                                                                                   394 AA
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                                                                   356 YEDFDVDA-AARGMAFERLDQLAMDHLLGAR
                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                             Ampullariella sp. (strain 3876)
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HSSP; P12851; 4XIM.
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                                                                                                                                                                                                 XYLA_AMPSP
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XYLA_AMPSP
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Best Local Similarity 65.7%
Matches 257; Conservative
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PIR; S16214; S16214; S16214, S16214, SPB; IXIA; 15-JAN-91.

PPB; AIXA; 15-JAN-91.

PPB; AIXA; 15-JAN-91.

PPB; AIXA; 15-JAN-91.

PPB; AIXA; 15-JUL-93.

PPB; IXIA; 15-JUL-93.

PPB; IXI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomyces and Arthrobacter.";
Protein Eng. 1:467-469(1987).
-!- CATALYTIC ACTIVITY. D-XYLOSE - D-XYLULOSE.
-!- COFACTOR: MAGNESIUM IS NECESSARY FOR THE ACTIVITY.
-!- SUBUNIT: HOMOTETRAMER.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC.
-!- SIMILARITY: BELONGS TO THE XYLOSE ISOMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
      295 IDGVWASAAGCMRNYLILKERAAAFRADPEVQEALRAARLDQLAEPTAADG--LQALLAD 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HENRICK K., COLLYER C.A., BLOW D.M.;
"Structures of D-xylose isomerase from Arthrobacter strain B3728
containing the inhibitors xylitol and D-sorbitol at 2.5-A and 2.3-A
Tesolution, respectively.";
J. Mol. Biol. 208:129-157(1989).
                                                       LFHIDLNGQSGIKYDQDLRFGAGDLRAAFWLVDLLESA----GWEGPRHFDFKPPRTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMITH C.A., RANGARAJAN M., HARTLEY B.S.;
D-YX10se (D-glucose) isomerase from Arthrobacter strain N.R.R.L.
B3728 Purification and properties.";
Biochem. J. 277:255-261(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE; 91307531.
LOVINY-ANDERTON T., SHAW P.C., SHIN M.K., HARTLEY B.S.;
LOVINY-ANDERTON T., SHAW P.C., SHIN M.K., HARTLEY B.S.;
"D-Xylose (D-glucose) isomerase from Arthrobacter strain N.R.R.L.
B3728 Gene clouing, sequence and expression.";
B10chem. J. 277:263-271(1991).
                                                                                                                                                                                                                                                                                                                                                                                                             Arthrobacter sp. (strain NRRL B3728).
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Micrococcineae; Micrococcaceae; Arthrobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 89220984.
HENRICK K., BLOW D.M., CARELL H.L., GLUSKER J.P.;
"Comparison of backbone structures of glucose isomerase from
                                                                                                                                                                                                                                                                                              XYLA_ARTS7 STANDARD; PRT; 394 AA. P12070; 01-0CT-1989 (Rel. 12, Created) 101-MG-1992 (Rel. 23, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) XYLOSE ISOMERASE (EC 5.3.1.5).
                                                                                                                                                                                  353 RTAYEDFDVDA-AARGMAFERLDQLAMDHLLGAR 385
                                                                                                                                                                                                    SEQUENCE OF 1-20, AND CHARACTERIZATION.
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P56681;
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Matches 228;
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ID XYLA_T
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MEDLINE; 91216978.
DEKKER K., YAMAGATA H., SAKAGUCHI K., UDAKA S.;
"Xylose (glucose) isomerase gene from the thermophile Thermus tharmophilus: cloning, sequencing, and comparison with other thermostable xylose isomerases.";
                                                                                                                                                                                                                                                                                                          62.9%; Score 1277; DB 1; Length 394; 62.5%; Pred. No. 6.6e-93; ive 52; Mismatches 85; Indels 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thermus aquaticus (subsp. thermophilus).
Bacteria; Thermus/Deinococcus group; Thermus group; Thermus
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Last sequence update)
Last annotation update)
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Matches 245; Conservative
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(Rel. 23,
(Rel. 23,
(Rel. 38,
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MEDLINE; 99264393.
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01-AUG-1992 (
15-JUL-1999 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isomerase, Pentose shunt; Xylose metabolism; Magnesium; 3D-structure. ACT_SITE 53 53 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
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CHANG C., PARK B.C., LEE D.-S., SUH S.W.;

"Crystal structures of thermostable xylose isomerases from Thermus caldophilus and Thermus thermophilus: possible structural determinants of thermostability.";

J. Mol. Biol. 288:623-634(1999).

-! CATALYTIC ACTIVITY: D-XYLOSE = D-XYLULOSE.

-! CATALYTIC ACTIVITY: D-XYLOSE = D-XYLULOSE.

-! SUBUNIT: HOMOTETRAMER.

-! SUBCELLULAR LOCATION: CYTOPLASMIC.

-! SUBLESTIVE BELONGS TO THE XYLOSE ISOMERASE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAGNESIUM (BY SIMILARITY).
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(Rel. 38, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00172; XYLOSE_ISOMERASE_1; 1.
PROSITE; PS00173; XYLOSE_ISOMERASE_2; 1.
PFAM; PF00259; Xylose_1som; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                          IDLAVELGAKVYVAWGGREGAESGAAKDVRAALDRMKEAFDLLGEYVTSQGYDIRFAIEP 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KPNEPRGDILLPTIGHALAFIERLERPELYGVNPEVGHEQMAGLNFPHGIAQALWAGKLF 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PDB: 1BXC: 16-FEB-99.
PROSITE: PS00172: XVLOSE_ISOMERASE_1: 1.
PROSITE: PS00173: XVLOSE_ISOMERASE_2: 1.
PROSITE: PS00173: XVLOSE_ISOMERASE_2: 1.
ACT_SITE: 53 53 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             302 ARGCMRTYLILKERAEAFREDPEVKELLAAYYQEDPAALPLMDPYSHEKAEALKRAELPL 361
                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                               3 YQPTPEDRFTFGLWTVGWQGRDPFGDATRPALDPVDV-QRLAELGAYGVTFHDDDLIPFG 61
                                                                                                                                             CHANG C., SONG H.K., PARK B.C., LEE D.-S., SUH S.W.;
At thermostable xylose isomerase from Thermus caldophilus: biochen characterization, crystallization and preliminary X-ray analysis. Acta Crystallogr. D 55:294-296(1999).
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                                                                                                                                                                                                                                                                                                                                                               5
                      caldophilus).
                                                                                                                                                                                                                                                                                                                                            54.2%; Score 1100; DB 1; Length 387;
57.5%; Pred. No. 4.7e-79;
tive 43; Mismatches 119; Indels
                                                                                                                                                                                                                                                                                MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY)
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
annotation update)
                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS)
                                                   CRYSTALLIZATION, AND CHARACTERIZATION
                        Thermus aquaticus (subsp. caldophilus
Bacteria; Thermus/Deinococcus group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :| || || || || || || || || || || || || EAKRHRGYALERLDQLAVEYLLGVRG 387
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15-JUL-1999 (Rel. 38, Last an
XYLOSE ISOMERASE (EC 5.3.1.5)
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hes 222; Conserv
                                                                    MEDLINE; 99190865.
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MEDLINE; 99264393.
                                                            STRAIN-GK24
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Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics. Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45 RFSVAYWHTFDQRLVDPFGDGTAQRPYDHITDPMDLALAKVDAAFEFYHKLGVDYLCFHD 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55 DDLIPFGASDTEREAHVKRFRQALD-----ATGMTVPMATINLFTHPVFKAGAFTAND 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54
                                                                                                                                           Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae; Lactobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  282 QHEIRVAREANLLGSLDANGGDKLIGWDID-EFPSDLYEATAAMYEVVEN-GSIGPRGGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 RFTFGLW-TVGWQGRDPFGDAT--RP---ALDPVDV------QRLAELGAYGVTFHD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               168 VTSQGYDIRFALEPKPNEPRGDILLPTIGHALAFIERLERPELYGVNPEVGHEQMAGLNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           228 PHGIAQALWAGKLFHIDLN-GQSGIKYDQDLRFGAGDLRAAFWLVDLLESAGWEGPR---
                                                                                                                                                                                                                                                            77;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61; Mismatches 150;
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Pred, No. 5.7e-19;
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                                                        update)
449
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MAGNESIUM
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MAGNESIUM
                                  01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
XYLOSE ISOMBRASE (EC 5.3.1.5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, M57384; AAA25258.1; -.
PIR; S18561; S18561.
HSSP, P19148; 1A0C.
PROSITE; PS00172; XXLOSE_ISOMERASE_1;
PROSITE; PS00173; XXLOSE_ISOMERASE_2;
PFAM; PF00259; Xylose_1som: 1.
PRT;
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STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    270
298
342
                                                                                                                                   Lactobacillus pentosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isomerase; Pentose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          449 AA;
                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                               MEDLINE; 92079891.
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270
298
342
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XYLA_LACPE
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Best Local Similarity
Matches 109; Conserv
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MEDLINE; 98320588.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tetragenococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            XYLA_TETHA
082845;
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HFDFKPPRTE-----DIDGVWASAAGCMRNYLILKERAAAFRADPEVQEALRAARL 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCHELER A., RYGUS T., ALLMANSBERGER R., HILLEN W.; "Molecular cloning, structure, promoters and regulatory elements for transcription of the Bacillus licheniformis encoded regulon for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 RFTFGLW-TVGWQGRDPFGDAT-----RPALDPVDVQR------LAELGAYGVTFHD 54
                                      340 NFDAKPRESSFAANDLFYGHIVGIDTFAAG-LRVALKMKQ-------
                                                                                 335 DQLAEPTAADG-LQALLADRTAYEDFDVDAAAR---GMA-FERLDQLAMD 379
                                                                                                                            ------DGFLEKLVADR--YSSYQSGVGAEIEAGTADFKSLESYAID 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16.2%; Score 329; DB 1; Length 448; 29.5%; Pred. No. 1.3e-18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55; Mismatches 160;
                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
XYLOSE ISOMERASE (EC 5.3.1.5).
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EMBL; X57601; CAA40827.1; -.
PROSITE; P800172; XXLOSE_ISOMERASE_1; 1.
PROSITE; PS00173; XXLOSE_ISOMERASE_2; 1.
PRAM; PF00259; Xylose_1som; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arch. Microbiol. 155:526-534(1991).
                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 29.5% Matches 104; Conservative
                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                             Bacillus licheniformis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-DSM13;
MEDLINE; 92061500.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tetragenococcus halophilus (Pediococcus halophilus).
Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
                                            RRYALRKTIRNIDLAVELGAKVYVAWGGREGAESGAAKDVRAALDRMKEAFDLLGEYVTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
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XYLOSE ISOMERASE (EC 5.3.1.5).
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105 ANDRAVRRYALRKTIRNIDLAVELGAKVYVAWGGREGAESGAAKDVRAALDRMKEAFDLL 164
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	A, Titl	le: A	Nucleot	ide se	guence	of	the	xylose isomerase gene fr	rom Streptomyces	es violaced
÷	A; Rete	erencessic	ce numb	436	1436;	MOID	68:	116633		
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	A; Cros	ss-re	eferenc	this s	(BL:X12)	816; e, 1	NID	304. of t	1; PID:948005 he mature prote	ein, was co
	C; Gene	etičs			•				•	
	C) COM	plex	homot	etrame	Ħ					
	A; Desc	cript	tion: c	atalyz	es iso	meri	zati	ion of the aldopentose D	-xylose to the	2-ketopent
	A; Patl C; Supe	hway: erfam	xylos	e meta	bolism isomera	386				
	C; Keys F; 2-38	words 89/Pr	s: homo roduct:	xylos	ner; in	trameras	olec e #s	st '5	omerase; magnes	sium; xylos
	F,54,	57/AC	ctive s	itte: H	its, As	# cr	tatu	is predicted	7	
	F; 181, F; 217,	,217,	, 245, 28	7/Bind	ling si	t t t t t t t t t t t t t t t t t t t	magn	F;181.217,245.287/Binding site: magnesium (Glu, Glu, Asp, Asp) F;217,220,255,257/Binding site: magnesium (Glu, His, Asp, Asp)	#status pr #status pr	edicted edicted
	One	ry Ma	LC.		93	.38	0)	1892.5; D	jth 389;	
	Best I Matche	t Loca ches	cal Simila 359; Co	ari ons	ty 92 ervative	۳. _ص	15;	No. 3e-137; smatches 12; In	en so	2;
	٥x	н	MNYOPT	PEDRFT	FGLWTV	GWOG	RDPE	GDATRPALDPVD-VQRLAELGAY	SVIFHDDDLIP 59	
	QC	Н	MSFQPT	PEDKET	FGLWTV	SWOG	RDPF	MSFQPTPEDKFTFGLWTVGWQGRDPFGDATRPALDPVETVQRLAELGAYGVTFHDDDLI	SVTFHDDDLIP 60	
	οy	9	FGASDT	EREAHY	KREROA	LDAT	GMTV	FGASDTEREAHVKRFRQALDATGWTVPWATTNLFTHPVFKAGAFTANDRAVRRALIKTI	11	6
	qa	61	FGSSDT	ERESHI	KRFRQA	LDAT	GMTV	<i>P</i> MATTNLFTHPVFKDGGFTANDRI	12	0
	οy	120	RNIDLA	VELGAR	CVYVAWG	GREG	AESG	RNIDLAVELGAKVYVAWGGREGAESGAAKDVRAALDRWKEAFDLLGEYVTSQGYDIRFAI	17	Ø
	qq	121	RNIDLA	AELGAK	CTYVAWG	GREG	AESG	GAKDVRDALDRMKEAFDLLGEYV	18	0
	Qy	180	EPKPNE	PRGDIL	LPTIGH	ALAF	IERI	EPKPNEPRGDILLPTIGHALAFIERLERPELYGVNPEVGHEQMAGLNFPHGIAQALWAGK	23	6
	g G	181	EPKPNE	PRGDIL	LPTVGH	ALAF	IERI	LERPELYGVNPEVGHEQMAGLNFP	24	0
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A; Description: catalyzes isomerization of the aldopentose D-xylose to the 2-ketopento
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               xylose isomerase (EC 5.3.1.5) - Streptomyces olivochromogenes
C; Species: Streptomyces olivochromogenes
C; Species: Streptomyces olivochromogenes
C; Date: 25.Feb-1994 #sequence_revision 06-Dec-1996 #text_change 10-Sep-1999
C; Accession: S28986
R; Farber, G.K.; Glasfeld, A.; Tiraby, G.; Ringe, D.; Petsko, G.A.
Biochemistry 28, 7289-7297, 1989
A; Title: Crystallographic studies of the mechanism of xylose isomerase.
A; Reference number: S28986; MUID: 90057422
A; Contents: X-ray crystallography, 3.0 angstroms
A; Accession: S28986; MUID: 90057422
A; Contents: Tay crystallography, 3.0 angstroms
A; Residues: 1-389 cFRAN
A; Residues: 1-389 cFRAN
A; Residues: 1-389 cFRAN
A; Reference number: A50637; PDB: 3XIA
A; Reference number: A50637; PDB: 3XIA
A; Contents: annotation; X-ray crystallography, 3.0 angstroms, residues 2-378
C; Complex: homodimer
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                                                RNIDLAVELGAETYVAWGGREGAESGGAKDVRDALDRMKEAFDLLGEYVTSQGYDIRFAI
                                                                                                       EPKPNEPRGDILLPTIGHALAFIERLERPELYGVNPEVGHEQMAGLNFPHGIAQALWAGK
                                                                                                                                                             EPKPNEPRGDILLPTVGHALAFIERLERPELYGVNPEVGHEQMAGLNFPHGIAQALWAGK
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National stoomersee (RC 5.3.1.5) - Streptomyces rubiginosus
National stoomersee (RC 5.3.1.5) - Streptomyces rubiginosus
C. Species: Streptomyces rubiginosus
C. Species: Streptomyces rubiginosus
National Nation
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241 LFHIDLNGQSGIKYDQDLRFGAGDLRAAFWLVDLLESAGYEGPRHFDFKPPRTEDFDGVW 300
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                                                                                ASAAGCMRNYLILKERAAAFRADPEVQEALRAARLDQLAEPTAADGLQALLADRTAYEDF
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Best Local Similarity 92.3%; Pred. No. 4.5e-136;
Matches 358; Conservative 14; Mismatches 14;
                                                                                                                                                             DVDAAARGMA--FERLDQLAMDHLLGARG 386
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A; Reference number: JN0086; MUID:91136786
A; Accession: JN0086
A; Accession: JN0086
A; Molecule type: DNA
A; Residues: 1-394 < KIX>
C; Comment: Phe-26, Phe-94, and Trp-136 have been demonstrated to be involved in facil
C; Competics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Description: catalyzes isomerization of the aldopentose D-xylose to the 2-ketopento
C; Complex: homotetramer
C; Function:
A; Description: catalyzes isomerization of the aldopentose D-xylose to the 2-ketopento
C; Superfamily: xylose metabolism
C; Superfamily: xylose isomerase #status predicted < AMT>
F; 2-394/Product: xylose isomerase #status predicted
C; Keywords: homotetramer; intramolecular oxidoreductase; isomerase; magnesium; xylose
F; 2-394/Product: xylose isomerase #status predicted
F; 90, 182/Binding site: substrate (Thr. Lys) #status predicted
F; 180, 216, 219, 254, 256/Binding site: magnesium (Glu, His, Asp, Asp) #status predicted
F; 216, 219, 254, 256/Binding site: magnesium (Glu, His, Asp, Asp) Asp) #status predicted
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Nylternate names: xylose ketol-isomerase
C;Species: Ampullariella sp.
C;Species: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 06-Dec-1996
C;Accession: Allower, A.A.; Kawasaki, G.H.; Insley, M.Y.; O'Hara, P.J.
J. Bacteriol. 169, 612-618, 1987
A;Title: Sequence of the Ampullariella sp. strain 3876 gene coding for xylose isomera A;Reference number: A27756; MUID:87109047
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A;Cross-references: GB:M15050
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C; Complex: homotetramer
C; Function:
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C;Species: Streptomyces diastaticus
C;Species: Streptomyces diastaticus
C;Species: Streptomyces diastaticus
C;Species: Streptomyces diastaticus
C;Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 06-Dec-1996
C;Accession: JC1031
E;Wang, Y. 2.; Huang, Z.; Dai, X. H.; Liu, J.; Cui, T.; Niu, L. W.; Wang, C.; Xu, X.
Chinese J. Biotechnol. 10, 118-123, 1994
A;Title: DNA sequence of xylose isomerase gene from Streptomyces diastaticus No.7 strain
A;Reference number: JC1031
A;Reference number: JC1031
A;Molecule type: DNA
A;Residues: 1-388 cWAN>
C;Superfamily: xylose isomerase
C;Keywords: intramolecular oxidoreductase; isomerase
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N;Alternate names: xylose ketol-isomerase
C;Species: Streptomyces rochei
C;Decies: Streptomyces rochei
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 07-May-1999
C;Accession: JN0086
S;Kikuchi, T.; Itoh, Y.; Kasumi, T.; Fukazawa, C.
Agric. Biol. Chem: 54, 2469-2472, 1990
A;Title: Molecular cloning of the xylA gene encoding xylose isomerase from Streptomyces
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magnesium; xylose

Asp, Asp) #status experimental Asp, Asp) #status experimental

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A; Pathway: xylose meconorase
C; Superfamily: xylose isomerase
C; Keywords: homotetramer; intramolecular oxidoreductase; isomerase;
C; Keywords: homotetramer; intramolecular oxidoreductase;
E; 94,57/Active site: His, Asp #status experimental
F; 90,183/Binding site: substrate (Thr. Lys) #status experimental
F; 181,217,245,292/Binding site: magnesium (Glu, Glu, Asp, Asp) #stat
F; 217,220,255,257/Binding site: magnesium (Glu, His, Asp, Asp) #stat
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A; Molecule type: protein
                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                            Query Match
Best Local
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N. Alternate names: xylose ketch-lasomerase
C; patci 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 18-Jun-1999
C; patci 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 18-Jun-1999
C; Accession: SO5998
R; Mollecule xylose isomerase from Actinoplanes missouriensis: primary structure of the gene A; Fittle: xylose isomerase from Actinoplanes missouriensis: primary structure of the gene A; Accession: SO5998
A; Molecule type: DNA
A; Residues: 1-394 <AMO:
A; Residues: 1-394 <AMO:
A; Accession: SO5998
A; Molecule type: DNA
A; Accession: SO5998
A; Accession: SO5998
A; Accession: SO5998
A; Cross-references: EMBL:X16042; NID:938870; PIDN:CAA34164.1; PID:9580713
A; Molecule type: DNA
A; Cross-references: EMBL:X16042; NID:938870; PIDN:CAA34164.1; PID:9580713
A; Molecule type: DNA
A; Cross-references: EMBL:X16042; NID:938870; PIDN:CAA34164.1; PID:9580713
A; Molecule type: DNA
A; Molecule type: Ascention: A: Tay crystallography, 2.5 angstroms
C; Genetics: annotation; X-ray crystallography, 2.8 angstroms
C; Genetics: annotation; X-ray crystallography, 2.8 angstroms
C; Genetics: A; Saference number: A58417; MuID:89184498
A; Start codon: GTG
C; Complex: homotetramer
C; Function:
C; Function:
C; Function:
C; Function:
C; Function:
A; Description: catalyzes isomerization of the aldopentose to the 2-ketopentose
     the 2-ketopentose
A; Description: catalyzes isomerization of the aldopentose D-xylose to the 2-ketopentos A; Pathway: xylose metabolism
C; Superfamily: xylose isomerase isomerase isomerase; magnesium; xylose is 54,57/Active site: His, Asp #status predicted
F; 54,57/Active site: His, Asp #status predicted
F; 90,183/Binding site: substrate (Thr, Lys) #status predicted
F; 131,217,245,232/Binding site: magnesium (Glu, Glu, Asp, Asp) #status predicted
F; 217,220,255,257/Binding site: magnesium (Glu, His, Asp, Asp) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       295 IDGVWASAAGCMRNYLILKERAAAFRADPEVQEALRAARLDQLAEPTAADG--LQALLAD 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                FGASDIEREAHVKRFRQALDAIGMIVPMATINLFIHPVFKAGAFIANDRAVRKYALRKII 119
                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                            1 MNYOPTPEDRFTFGLWTVGWQGRDPFGDATRPALDPVD-VQRLAELGAYGVTFHDDDLIP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LFHIDLNGQSGIKYDQDLRFGAGDLRAAFWLVDLLESA-----GWEGPRHFDFKPPRTED
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                                                                                                                                                                                                                                                       Length 394;
                                                                                                                                                                                                                                                  Query Match
Bost Local Similarity 66.0%; Pred. No. 4.3e-96;
Matches 260; Conservative 46; Mismatches 79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RTAYEDFDVDA-AARGMAFERLDQLAMDHLLGAR 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181
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xylose somerase (EC 5.3.1.5) - Arthrobacter sp.

Xylose stomerase (EC 5.3.1.5) - Arthrobacter sp.

NiAlternate names: D-glucose isomerase
C; Species: Arthrobacter sp.
C; Species: Arthrobacter sp.
C; Species: Arthrobacter sp.
C; Species: Arthrobacter sp.
C; Date: 21 - Sha', Sl6212; S28154
R; Loviny-Anderton, T: Shaw, P.C.; Shin, M.K.; Hartley, B.S.
Bloochem. J. 277, 263-271, 1991
A; Title: D-Xylose (D-glucose) isomerase from Arthrobacter strain N.R.R.L. B3728. Gene
A; Recension: S16214
A; Molecule type: DNA
A; Residues: 1.355 < 4210.
A; Residues: 1.355 < 4210.
A; Residues: EMBL:X59466; NID:939058; PIDN:CAA42073.1; PID:939059
A; Experimental source: EMBL:X59466; NID:93728
B; Smith, C.A.; Rangarajan, M.; Hartley, B.S.
Bloochem. J. 277, 255-261, 1991
A; Title: D-Xylose (D-glucose) isomerase from Arthrobacter strain N.R.L. B3728. Puri
A; Residues: 2.21 < 4812
A; Residues: 2.21 < 4812
A; Residues: 2.21 < 4812
A; Molecule type: protein
A; Residues: 2.21 < 4812
A; Note: other peptide sequences were also determined
B; Siddiqui, K.S.; Rangarajan, M.; Hartley, B.S.; Kitmitto, A.; Panico, M.; Blench, I. B; State: Arthrobacter D-xylose isomerase: partial proteolysis with thermolysin.
B; A; Ritle: Arthrobacter D-xylose isomerase: partial proteolysis with thermolysin.
A; Residon content of the period of the content of t
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                                                                                                                                                                                                                                                                                                                                                                                                       RNIDLAVELGAKVYVAWGGREGAESGAAKDVRAALDRMKEAFDLLGEYVTSQGYDIRFAI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EPKPNEPRGDILLPTIGHALAFIERLERPELYGVNPEVGHEQMAGLNFPHGIAQALWAGK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LFHIDLNGQSGIKYDQDLRFGAGDLRAAFWLVDLLESA-----GWEGPRHFDFKPPRTED 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IDGVWASAAGCMRNYLILKERAAAFRADPEVQEALRAARLDQLAEPT--AADGLQALLAD 352
                                                                                               Gaps
                                                                                                                                                                            1 MNYQPTPEDRFTFGLWTVGWQGRDPFGDATRPALDPVD-VQRLAELGAYGVTFHDDDLIP 59
                                                                                                                                                                                                                                                                   1 MSVQATREDKFSFGLWTVGWQARDAFGDATRTALDPVEAVHKLAEIGAYGITFHDDDLVP 60
                                                                                          <u>ن</u>
    Length 394;
                                                                                          Indels
Score 1351.5; DB 1; Pred. No. 6.1e-96; 51; Mismatches 76; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RTAYEDFDVDA-AARGMAFERLDQLAMDHLLGAR 385
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65.5%;
                                                                                          Matches 258; Conservative
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pentos

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C) Accession: S18561
R; Lokman, B.C.; van Santen, P.; Verdoes, J.C.; Kruese, J.; Leer, R.J.; Posno, M.; Pou Mol. Gen. Genet. 230, 161-169, 1991
A; Title: Organization and characterization of three genes involved in D-xylose catabo A; Reference number: S18560; MUID:92079891
A; Accession: S18561
A; Cossion: S1
                                                                                                    from the thermophile Thermus thermophilus:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       metabolism
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                                                                                                                                                                                                                                                                                               magnesium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HIDLNGQSGIKYDQDLRFGAGDLRAAFWLVDLLESAGWEGPRHFDFKPPRTEDIDGVWAS 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Asp, Asp) #status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 ASDTEREAHVKRFRQALDATGMTVPMATINLFTHPVFKAGAFTANDRAVRRYALRKTIRN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IDLAVELGAKVYVAWGGREGAESGAAKDVRAALDRMKEAFDLLGEYVTSQGYDIRFAIEP
   C;Accession: A39404
R;Dekker, K.; Yamagata, H.; Sakaguchi, K.; Udaka, S.
J. Bacteriol. 173, 3078-3083, 1991
A;Title: Xylose (glucose) isomerase gene from the thermophile Thermu A;Reference number: A39404; MUID:91216978
A;Accession: A39404
A;Molecule type: DNA
A;Residues: 1-387 < CDEK>
C;Superfamily: Xylose isomerase
C;Keywords: homotetramer; intramolecular oxidoreductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77;
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                                                                                                                                                                                                                                                                                                                                                                                   Length 387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               xylose isomerase (EC 5.3.1.5) - Lactobacillus pentosus
C;Species: Lactobacillus pentosus
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Superfamily: xylose isomerase
C; Keywords: intramolecular oxidoreductase; isomerase;
F;103,106/Active site: His, Asp #status predicted
F;143,236/Bunding site: substrate (Thr. Lys) #status p
F;234,270,298,342/Binding site: magnesium (Glu, Glu, A
                                                                                                                                                                                                                                                                                                                                                                            ; Score 1127; DB 2;
; Pred. No. 8.3e-79;
43; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             386
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                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 58.5
Matches 228; Conservative
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Best Local Simi
Matches 122;
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A:Residues: 337-348 <SID>
R:Residues: 337-348 <SID>
R:Residues: 337-348 <SID>
R:Reference to the Brookhaven Protein Data Bank, July 1989
A:Reference number: A50703; PDB:4XIA
A:Contents: annotation; X-ray crystallography, 2.3 angstroms, with D-sorbitol, residues
R:Henrick, K.; Collyer, C.A.: Blow, D.M.
A:Contents: annotation; X-ray crystallography, 2.3 angstroms
R:Henrick, K.; Collyer, C.A.: Henrick, K.; Blow, D.M.
A:Title: Structures of D-xylose isomerase from Arthrobacter strain B3728 containing the A:Reference number: A58418; MUID:8956243
A:Title: Structures of D-xylose isomerase from Arthrobacter strain B3728 containing the A:Reference number: A58418; MUID:8956243
A:Title: Structures of D-xylose isomerase from Arthrobacter strain B3728 containing the A:Reference number: A51428; PDB:1XLC
A:Contents: annotation; X-ray crystallography, 2.5 angstroms, with D-xylose/xylulose and R:Collyer, C.A.: Henrick, K.; Blow, D.M.
A:Reference number: A51428; PDB:1XLC
A:Contents: annotation; X-ray crystallography, 2.5 angstroms
C:Conplex: A:Reference number: A54419; MUID:90204542
A:Contents: annotation: X-ray crystallography, 2.5 angstroms
C:Conplex: homotetramer
C:Function:
A:Petence xyl A
C:Conplex: Nylose asomerase status experimental
C:Function:
A:Description: catalyzes isomerization of the aldopentose D-xylose to the 2-ketopentose
C:Revords: xylose asomerase
C:Revords: A:Pethamer: intramolecular oxidoreductase; isomerase; magnesium; xylose methabolian
C:Pubertion:
C:Pubert
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LFHIDLNGQSGIKYDQDLRFGAGDLRAAFWLVDLLESA-----GWEGPRHFDFKPPRTE 293
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Best Local Similarity
Matches 246; Conserv
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Nature 399, 323-329, 1999
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A; Residues: 1-444 <ARN>
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                                                                                                                                                                                                                                                       C, Accession: A72225
R; Nelson, K.E.; Clay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: TM1667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
140806
xylose isomerase (EC 5.3.1.5) - Clostridium thermosaccharolyticum
c; Species: Clostridium thermosaccharolyticum,
C; Species: Clostridium thermosaccharolyticum,
C; Species: Clostridium thermosaccharolyticum,
C; Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 16-Jul-1999
C; Accession: 140806
R; Maeden, P.G.; Aduse-Opoku, J; Reizer, J; Reizer, A.; Lanceman, Y.A.; Martin, M.F.; M
Gane 141, 97-101, 1994
A; Title: The xylose isomerase-encoding gene (xylA) of Clostridium thermosaccharolyticum:
A; Reference number: 140806; MUID: 94215896
A; Recession: 140806
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: cferences: GB: M91248; NID: g144787; PIDN: AAA79035.1; PID: g144788
C; Genetics:
A; Gene: xylA
C; Superfamily: xylose isomerase
C; Ksywords: intramolecular oxidoreductase; isomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14;
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                                                                                                                                                                                                                                                                                                       QHEIRVAREANLLGSLDANQGDKLIGWDID-EFPSDLYEATAAMYEVVEN-GSIGPRGGL 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DVFAYSAAQVKKALEITKELGGQNYVFWGGREGYETLLNTDMELELDNFARFLHMAVDYA 220
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                                                                                                                                                                                                                                                                                                                                          HFDFKPPRTE------DIDGVWASAAGCMRNYLLLKERAAFRADPEVQEALRAARL 334
                               RFSVAYWHTFDQRLVDPFGDGTAQRPYDHITDPMDLALAKVDAAFEFYHKLGVDYLCFHD 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                               RDLAPEG -- DILREIN-RNLDKVIDKIVDYQKQTGMKVLWNTSNMFINPRFVAGAATSPD
                                                                                                                                                        RFTFGLW-TVGWQGRDPFGDAT--RP---ALDPVDVQR-----LAELGAYGVTFHD
                                                                 DDLIPFGASDTEREAHVKRFRQALD-----ATGMTVPMATTNLFTHPVFKAGAFTAND
                                                                                                                                                                                                                                                                         PHGIAQALWAGKLFHIDLN-GQSGIKYDQDLRFGAGDLRAAFWLVDLLESAGWEGPR---
 --- QRLAELGAYGVTFHD
                                                                                                                                    RAVRRYALRKTIRNIDLAVELGAKVYVAWGGREGAESGAAKDVRAALDRMKEAFDLLGEY
                                                                                                                                                                                                      VISQCYDIRFAIEPKPNEPRGDILLPTIGHALAFIERLERPELYGVNPEVGHEQMAGLNF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tch 15.7%; Score 318; DB 2; Length 43 al Similarity 27.5%; Pred. No. 5.7e-17; 111; Conservative 61; Mismatches 168; Indels
RFTFGLW-TVGWQGRDPFGDAT--RP---ALDPVDV-
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Best Local S
Matches 111
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A.Experimental source: strain MSB8
C.Ganatine:
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A;Accession: A72225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RiNelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hi
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16;
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N;Alternate names: glucose isomerase A
C;Species: Lactobacillus brevis
C;Date: 04-Dec-1992 #seque brevision 04-Dec-1992 #text_change 16-Jul-1999
C;Accession: JC1137; PS0435
                                                                                                                                                                                                                                                                                                                                                                                                                                    xylose isomerase - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Spate: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HGIAQALWAGKLFHIDLN-GQSGIKYDQDLRFGAGDLRAAFWLVDLLESAGW-EGPRHFD 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      169 TSQGYDIRFAIEPKPNEPRGDILLPTIGHALAFIERLERPELYGVNPEVGHEQMAGLNFP 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           221 KKIGFTGQFLIEPKPKEPTKHQYDFDVATAYAFLKNHGLDEYFKFNIEANHATLAGHTFQ 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       281 HELRMARILGKLGSIDANQGDLLLGWDTD-QFPTNIYDTTLAMYEVIKAGGFTKGGLNFD 339
                                                                              ---AEFDKF 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43 KFSVAFWHTFVNEGRDPFGDPTAERPWNRFSDPMDKAFARVDALFEFCEKLNIEYFCFHD 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55 DDLIPFGASDTEREAH-----VKRFRQALDATGMTVPMATTNLFTHPVFKAGAFTANDR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            340 AKVRRASYKVEDLFIGHIAGMDTFALGFKIAYKLAKDGV----FDKFIEEKYRSFKEGIG 395
287 FKPPRT----ED-----IDGVWASAAGCMRNYLILKERAAAFRADPEVQEALRAARLDQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 RFTFGLW-TVGWQGRDPFGDAT--RP---ALDPVD-----VQRLAE----LGAYGVTFHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 AVRRYALRKTIRNIDLAVELGAKVYVAWGGREGAESGAAKDVRAALDRMKEAFDLLGEYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  287 FKPPR----TED----IDGVWASAAGCMRNYLILKERAAAFRADPEVQEALRAAR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              334 LDQLAEPTAADGLQALLADRTAYEDFDVDAAARGMAFERLDQLAMDHLL 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEIVEGKTDFEKLEEYIIDK---EDIELPSGKQ----EYLESLLNSYIV 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 15.6%; Score 317; DB 2; Length 44 Best Local Similarity 28.1%; Pred. No. 6.9e-17; Matches 115; Conservative 67; Mismatches 177; Indels
                                                                                                                                                                                                         338 AEPTAADGLQALLADRTAYED-FDVDAAARGMAFERLDQLAMDH
                                                                      340 AKVRRASFEPEDLFLGHIAGMDAFAKGFKVAYKLVKD---
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Gaps

31;

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xylose isomerase (EC 5.3.1.5) - Thermoanaerobacterium thermosulfurigenes
N.Alternate names: xylose ketol-isomerase
C;Species: Thermoanaerobacterium thermosulfurigenes
C;Date: 30-Jun-1992 **sequence_revision 30-Jun-1992 **text_change 18-Jun-1999
C;Accession: A36598; Si5119
R;Lee, C.; Bagdasarian, M.; Meng, M.; Zeikus, J.G.
J. Biol. Chem. 265, 19082-19090, 1990
A;Title: Catalytic mechanism of xylose (glucose) isomerase from Clostridium thermosul A;Reference number: A36598; MUID:91033437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Pathway: xylose metabolism
C; Superfamily: xylose isomerase
C; Keywords: homotetramer; intramolecular oxidoreductase; isomerase; magnesium; xylose
F; 101, 104/Active site: His, Asp #status predicted
F; 141, 234, Painding site: substrate (Thr. 1ys) #status predicted
F; 232, 268, 296, 339/Binding site: magnesium (Glu, Glu, Asp, Asp) #status predicted
F; 268, 271, 307, 309/Binding site: magnesium (Glu, His, Asp, Asp) #status predicted
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A; Residues: 1-439 <LEED
A; Residues: 1-430 <LEED
A; Cross-references: GB:J05650; NID:g144929; PIDN:AAA23285.1; PID:g144930
B; Cross-references: GB:J05650; NID:g144929; PIDN:AAA23285.1; PID:g144930
B; Cross-references: GB:J05650; NID:g144929; PIDN:AAA23285.1; PID:g144930
B; Cross-reference number: S15119; MUID:g144536
A; Accession: S15119; MUID:g1144536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Note: the sequence from page 568 is inconsistent with that from page 565 in having A;Note: the source is given as Clostridium thermosulfurogenes
                  Asp, Asp) #status predicted
                                                                                                                                                                                                                                                                                                                               41 RFSVAYWHTFTADLSDPFGVGVAERDWDSLDEMEKAKARVEAIFEFMEKTRIDYFCFHDV 100
                                                                                                                                                                                                                                                                                                                                                                                                     DLIPFGASDTEREAH----VKRFRQALDATGMTVPMATTNLFTHPVFKAGAFTANDRAVR 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RYALRKTIRNIDLAVELGAKVYVAWGGREGAESGAAKDVRAALDRMKEAFDLLGEYVTSQ 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GYDIRFAIEPKPNEPRGDILLPTIGHALAFIERLERPELYGVNPEVGHEQMAGLNFPHGI 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISPEGASLKESNENLDIIVELIKEKMDQTGKKLLWNTTNNFTHERFVHGAATSSNAEVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       232 AQALWAGKLFHIDLN-GQSGIKYDQDLRFGAGDLRAAFWLVDLLESAGW-EGPRHFDFKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 310.5; DB 1; Length 439;
Pred. No. 2.1e-16;
                                                                                                                   Length 439;
                                                                                                                                                                                         Indels
                                                                                                                   Query Match 15.4%; Score 312.5; DB 2; Best Local Similarity 29.6%; Pred. No. 1.5e-16; Matches 99; Conservative 52; Mismatches 152;
                                                                                                                                                                                                                                                            10 RFTFGLW-TVGWQGRDPFG-DATRPALDPVDVQRLAELGAYGV-
              F;229,265,293,335/Binding site: magnesium (Glu, Glu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              290 PRT----ED----IDGVWASAAGCMRNYLILKE 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 339 RRISFKQEDLILTHIAGMDTFALGLRVAYKMIED
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29.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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A; Title: Organization, promoter analysis and transcriptional regulation of the Staphyloc A; Reference number: S16529; MUID:91326026
A; Residues: 1-439 csiz>
A; Residues: 1-439 csiz>
A; Residues: 1-439 csiz>
A; Ross-references: EMBL:X57599; NID:948833; PIDN:CAA40824.1; PID:948835
A; Note: the sequence from Fig. 4 is inconsistent with that from Fig. 2 in having 247-Asp C; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
C; Keywords: intramolecular oxidoreductase; isomerase; magnesium; xylose metabolism F; 98,101/Active site: His, Asp #status predicted
F; 138,231/Binding site: substrate (Thr, Lys) #status predicted
R;Bor, Y.C.; Moraes, C.; Lee, S.P.; Crosby, W.L.; Sinskey, A.J.; Batt, C.A. Gene 114, 127-131, 1992

A.Title: Cloning and sequencing the Lactobacillus brevis gene encoding xylose isomerase. A.Feference number: JC1137; MUID:92267372

A:Accession: JC1137

A:Accession: JC1137

A:Accession: BORA

A:Residues: 1-49 CBRA

A:Residues: BORA

A:Residues: 1-49 CBRA

A:Residues: 1-46 CBRA

A:Accession: BORA

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A:Accession
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AVRRYALRKTIRNIDLAVELGAKVYVAWGGREGAESGAAKDVRAALDRMKEAFDLLGEYV 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TSQGYDIRFAIEPKPNEPRGDILLPTIGHALAFIERLERPELYGVNPEVGHEQMAGLNFP 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        223 NEIGFDAQMLLEPKPKEPTTHQYDFDAATTIAFWKEYDLDKDFKLNLEGNHANLAGHTYQ 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     341 FDAKPRRSAFAPEDLFLGHIVGMDSFAAGL-----RVAAAMKQDGFLDNLKADRYS 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 RFTFGLW-TVGWQGRDPFGDAT--RP---ALDPVDV------QRLAELGAYGVTFHD 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HGIAQALWAGKLFHIDIN-GQSGIKYDQDLRFGAGDLRAAFWLVDLLESAGWEGPR---H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63; Mismatches 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.5%; Score 314; DB 2; 28.9%; Pred. No. 1.2e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           336 QLAEPTAADGLQALLADRTAYEDFDVD 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SYKSGVGAD-IESGKADLKSLEAYAID 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 15.55
Best Local Similarity 28.99
Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45
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                                                                                                                                                                  221 KEIGFEGGFLIEPKPKEPTKHQYDFDVANVLAFLKKYDLDKYFKVNIEANHATLAFHDFQ 280
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 35; Gaps
                     10 RFTFGLW-TVGWQGRDPFGDAT--RP---ALDPVDVQR------LAELGAYGVTFHD 54
53; Mismatches 149; Indels
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